

Wild type hdm2 (17-125)

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OM protein - protein search, using sw model

Run on: January 27, 2005, 17:45:30 ; Search time 80.8 Seconds  
(without alignments)  
483.929 Million cell updates/sec

Title: US-10-822-254-2

Perfect score: 553

Sequence: 1 SQIPASEQETLVRPKPLLK.....NLVVNQESSDSGTSVSEN 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_23Sep04.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003s.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	553	100.0	284	2	AAR75494 Human dou
2	553	100.0	284	2	AAR75397 Human dou
3	553	100.0	491	2	AAR42175 Human MDM
4	553	100.0	491	2	AAR76696 Human MDM
5	553	100.0	491	2	AAR70787 Human MDM
6	553	100.0	491	2	AAR75463 Human MDM
7	553	100.0	491	2	AAR13380 Human MDM
8	553	100.0	491	2	AAR13600 Murine do
9	553	100.0	491	2	AAR48241 Human MDM
10	553	100.0	491	2	AAR57241 Human MDM
11	553	100.0	491	2	AAR42879 Amino aci
12	553	100.0	491	2	AAR42971 Amino aci
13	553	100.0	491	2	AAR4304 Human MDM
14	553	100.0	491	3	AAR96567 MDM2 onco
15	553	100.0	491	4	AAR48284 Human MDM
16	553	100.0	491	5	AAR22654 Human Rin
17	553	100.0	491	5	AAR22698 Human Rin
18	553	100.0	491	5	AAR25913 Human dou
19	553	100.0	491	5	AAR15376 Human Dm2
20	553	100.0	491	7	ADD21815 Human mdm
21	553	100.0	491	7	ADBE61562 Human Pro
22	553	100.0	491	8	ADL23893 Human E3
23	553	100.0	491	8	ADO52353 Human p53
24	553	100.0	491	8	ADP12593 Protein e
25	553	100.0	491	8	ADN71936 MDM2 prot

ALIGNMENTS

RESULT 1

AAR75494

ID AAR75494 standard; protein; 284 AA.

XX AAR75494;

AC AAR75494;

XX 02-FEB-1996 (first entry)

XX Human double minute 2 (hdm-2) antibody-binding region fragment 1.

XX Human double minute gene 2; hdm-2; antibody binding region; antigen;

XX Human double minute gene 2; hdm-2; antibody binding region; antigen;

XX cancer; sarcoma; rhabdomyosarcoma; diagnosis; immunoassay.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Region 1..284

XX /note= "amino acids 1-284 of hdm-2 gene product"

XX PN DE4339533-Al.

XX PD 14-JUN-1995.

XX PF 19-NOV-1993; 93DE-04339533.

XX PR 19-NOV-1993; 93DE-04339533.

XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX Zentgraf H, Klein R, Frey M, Martens R;

XX WPI; 1995-216248/29.

XX N-PSDB; AAQ92515.

XX Detection of human double minute gene 2 (hdm-2) antibodies - by

XX incubation with new hdm-2 or antibody-binding hdm-2 fragments; useful in

XX the detection of specific cancers.

XX Claim 11; Fig 1; 12pp; German.

XX Fragments contg. amino acids 1-284, 58-284 and 58-491 of the hdm-2 (human

XX double minute 2) gene product are claimed. The overlapping protein

XX fragments contain binding regions for hdm-2- specific antibodies and are

XX useful for identifying such antibodies in a claimed immunoassay method.

XX The presence of anti-hdm-2 antibodies is diagnostic of certain forms of

XX cancer, e.g. rhabdomyosarcoma

XX Sequence 284 AA;

SQ

wild type Hdm2

```
Query Match      100.0%; Score 553; DB 2; Length 284;
Best Local Similarity 100.0%; Pred. No. 3.6e-64;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVPRPKLLKLLKLSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 60
DB 17 SQIPASEQETLVPRPKLLKLLKLSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDLLGLDFGVPSFVKHHRKIYTMIRNLVVVNQESSDGSSTSVSEN 109
DB 77 CSNDLLGLDFGVPSFVKHHRKIYTMIRNLVVVNQESSDGSSTSVSEN 125

RESULT 2
AAR75397
ID AAR75397 standard; protein; 284 AA.
XX
AC AAR75397;
XX
DT 25-MAR-2003 (revised)
DT 25-JAN-1996 (first entry)
XX
DE Human double minute 2 (hdm-2) antibody-binding region fragment 1.
XX
KW Human double minute gene 2; hdm-2; antibody binding region; antigen;
KW cancer; sarcoma; rhabdomyosarcoma; diagnosis.
XX
OS Homo sapiens.
XX
FH Key
FT Region
FT 1..284
FN DE4345249-A1.
XX
XX 24-MAY-1995.
XX
PF 19-NOV-1993; 93DE-04345249.
XX
PR 19-NOV-1993; 93DE-04339533.
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI Zentgraf H, Klein R, Frey M, Martens R;
XX
WPI; 1995-195167/26.
DR N-PSDB; AAQ87261.
XX
PT New hdm-2 fragments contg. antibody binding region - used to detect
PT specific antibodies for diagnosis of cancers, also new DNA sequences
PT encoding them.
XX
PS Claim 2; Fig 1; 11pp; German.
XX
CC Fragments contg. amino acids 1-284, 58-284 and 58-491 of the hdm-2 (human
CC double minute 2) gene product are claimed. The overlapping protein
CC fragments contain binding regions for hdm-2- specific antibodies and are
CC useful for identifying such antibodies. The presence of anti-hdm-2
CC antibodies is diagnostic of certain forms of cancer, e.g.
CC rhabdomyosarcoma. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 284 AA;
Query Match      100.0%; Score 553; DB 2; Length 284;
Best Local Similarity 100.0%; Pred. No. 3.6e-64;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVPRPKLLKLLKLSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 60
DB 17 SQIPASEQETLVPRPKLLKLLKLSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDLLGLDFGVPSFVKHHRKIYTMIRNLVVVNQESSDGSSTSVSEN 109
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Db 77 CSNDLLGLDFGVPSFVKHHRKIYTMIRNLVVVNQESSDGSSTSVSEN 125

RESULT 3
AAR42175
ID AAR42175 standard; protein; 491 AA.
XX
AC AAR42175;
XX
DT 25-MAR-2003 (revised)
DT 05-MAY-1994 (first entry)
XX
DE Human MDM2.
XX
KW p53 gene; tumour suppressor gene; regulation; cellular proliferation;
KW cellular transformation; carcinoma; human; tumour; MDM2; inhibition;
KW gene amplification.
XX
OS Homo sapiens.
XX
PN WO9320238-A2.
XX
PD 14-OCT-1993.
XX
PF 07-APR-1993; 93WO-US003199.
XX
PR 07-APR-1992; 92US-00867840.
PR 23-JUN-1992; 92US-00903103.
XX
PA (UYJO ) UNIV JOHNS HOPKINS.
XX
PI Burrell M, Hill DE, Kinzler KW, Vogelstein B;
XX
WPI; 1993-336944/42.
DR N-PSDB; AAQ49891.
XX
XX Diagnosing neoplasia from amplification of MDM2 gene - or elevated gene
XX expression, also new DNA, MDM2 protein, antibodies and treatment of
XX sarcoma by inhibiting MDM2 expression.
XX
PS Claim 19; Fig 1; 75pp; English.
XX
XX This sequence is encoded by the MDM2 gene. Amplification of the MDM2 gene
XX is diagnostic of neoplasia or the potential for neoplasia. The protein
XX encoded by this gene interacts with the product of the p53 gene. p53 is a
XX tumour suppressor gene and encodes a protein which appears to be a member
XX of a group of proteins which regulate normal cellular proliferation and
XX suppression of cellular transformation. Inactivation of the p53 gene has
XX been implicated in the formation, or progression of a wide variety of
XX carcinoma. Polypeptides containing at least amino acids 13-41 of p53, or
XX the DNA encoding these, may be used to inhibit the growth of tumour cells
XX containing MDM2 gene amplification. (Updated on 25-MAR-2003 to correct PN
XX field.)
XX
SQ Sequence 491 AA;
Query Match      100.0%; Score 553; DB 2; Length 491;
Best Local Similarity 100.0%; Pred. No. 7.6e-64;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVPRPKLLKLLKLSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 60
DB 17 SQIPASEQETLVPRPKLLKLLKLSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDLLGLDFGVPSFVKHHRKIYTMIRNLVVVNQESSDGSSTSVSEN 109
DB 77 CSNDLLGLDFGVPSFVKHHRKIYTMIRNLVVVNQESSDGSSTSVSEN 125

RESULT 4
AAR76696
ID AAR76696 standard; protein; 491 AA.
```

XX AC AAR76696;  
 XX 16-OCT-2003 (revised)  
 DT 01-NOV-1995 (first entry)  
 XX Human MDM2 protein.  
 XX MDM2; sarcoma; diagnostic; DNA probe.  
 XX Homo sapiens; (cell line CaCo-2).  
 XX US5420263-A.  
 XX 30-MAY-1995.  
 XX 07-APR-1993; 93US-00044619.  
 XX 07-APR-1992; 92US-00867840.  
 XX 23-JUN-1992; 92US-00903103.  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 XX Vogelstein B, Kinzler KW;  
 XX WPI; 1995-206312/27.  
 XX N-PSDB; AAQ94589.  
 XX New human MDM2 cDNA - used to develop prods. for use in the diagnosis and treatment of tumours.  
 XX Claim 1; Col 23-26; 34pp; English.  
 XX The human MDM2 gene is genetically altered (i.e. amplified) in human tumour cells. The human MDM2 protein binds to human p53 and allows the cell to escape from p53-regulated growth. Detecting that the gene has become amplified or detecting increased gene product expression (using probes, proteins, antibodies and inhibitors) allows diagnosis and therapy of cancers such as colorectal carcinoma, lung cancer and chronic myelogenous leukaemia. (Updated on 16-OCT-2003 to standardise OS field)  
 XX Sequence 491 AA;  
 Query Match 100.0%; Score 553; DB 2; Length 491;  
 Best Local Similarity 100.0%; Pred. No. 7.6e-64;  
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTKKEVLFLYGLQYIMTKRLYDEKQOHIVY 60  
 DB 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTKKEVLFLYGLQYIMTKRLYDEKQOHIVY 76  
 QY 61 CSNDLLGLDFGVPSFSVKEHRKIYTMIRNLVVVNNQESSDSGTSVSEN 109  
 DB 77 CSNDLLGLDFGVPSFSVKEHRKIYTMIRNLVVVNNQESSDSGTSVSEN 125  
 RESULT 5  
 AAW07887  
 ID AAW07887 standard; protein; 491 AA.  
 XX AC AAW07887;  
 XX 25-MAR-2003 (revised)  
 DT 28-JAN-1997 (first entry)  
 XX Human MDM-2, involved in tumour-development.  
 XX p53; MDM-2; binding-inhibitor; identification; tumour; cancer; neoplasia;  
 XX antibody fusion protein; therapy.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers

FT Modified-site 166..169  
 FT /label= phosphorylation\_site  
 FT /note= "potential casein kinase II phosphorylation site"  
 FT Binding-site 181..185  
 FT /label= nuclear\_localisation\_signal  
 FT Modified-site 192..195  
 FT /label= phosphorylation\_site  
 FT /note= "potential casein kinase II phosphorylation site"  
 FT Domain 223..274  
 FT /label= acid\_activation\_domain  
 FT Modified-site 269..272  
 FT /label= phosphorylation\_site  
 FT /note= "potential casein kinase II phosphorylation site"  
 FT Modified-site 290..293  
 FT /label= phosphorylation\_site  
 FT /note= "potential casein kinase II phosphorylation site"  
 FT Domain 305..322  
 FT /label= metal\_binding\_site  
 FT Domain 461..478  
 FT /label= metal\_binding\_site  
 XX US5550023-A.  
 XX 27-AUG-1996.  
 XX 18-MAY-1994; 94US-00245500.  
 XX 07-APR-1992; 92US-00867840.  
 XX 23-JUN-1992; 92US-00903103.  
 XX 07-APR-1993; 93US-00044619.  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 XX Vogelstein B, Kinzler KW;  
 XX WPI; 1996-401591/40.  
 XX N-PSDB; AAT45151.  
 XX Identification of cpds. interfering with human MDM2/p53 binding - useful as therapeutic agents to treat human neoplastic cells.  
 XX Claim 26; Col 25-28; 36pp; English.  
 XX AAW07887 represents human MDM-2 derived from a human colon carcinoma cell line, CaCo-2, cDNA library. The MDM-2 protein is used in a method for identifying compounds that interfere with the binding of p53 and MDM-2. In binding the p53 protein, the MDM-2 protein releases a cell from p53-regulated growth, allowing cancers to develop. Therefore compounds identified as interfering with the binding of MDM-2 to p53 are potentially useful in the treatment of human neoplastic cells. In the method pref. one or both of the proteins is a fusion protein esp. with an antibody or antibody fragment which aids separation and identification.  
 XX (Updated on 25-MAR-2003 to correct PF field.)  
 XX Sequence 491 AA;  
 Query Match 100.0%; Score 553; DB 2; Length 491;  
 Best Local Similarity 100.0%; Pred. No. 7.6e-64;  
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTKKEVLFLYGLQYIMTKRLYDEKQOHIVY 60  
 DB 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTKKEVLFLYGLQYIMTKRLYDEKQOHIVY 76  
 QY 61 CSNDLLGLDFGVPSFSVKEHRKIYTMIRNLVVVNNQESSDSGTSVSEN 109  
 DB 77 CSNDLLGLDFGVPSFSVKEHRKIYTMIRNLVVVNNQESSDSGTSVSEN 125  
 RESULT 6  
 AAW15463  
 ID AAW15463 standard; protein; 491 AA.  
 XX

AC AAW15463;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 18-JUN-1997 (first entry)  
 XX  
 DE Human MDM2.  
 XX  
 KW Human; MDM2 protein; antibody; detection; cancer; diagnosis;  
 KW p53-regulated growth.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US5618921-A.  
 XX  
 PD 08-APR-1997.  
 XX  
 PF 17-FEB-1995; 95US-00390479.  
 XX  
 PR 07-APR-1992; 92US-00867840.  
 PR 23-JUN-1992; 92US-00903103.  
 PR 07-APR-1993; 93US-00044619.  
 XX  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 PI Vogelstein B, Kinzler KW, Burrell M, Hill DE;  
 XX  
 DR WPI; 1997-225474/20.  
 DR N-PSDB; AAT66410.  
 XX  
 PT Antibodies specific for human MDM2 protein - for diagnosis of cancer.  
 PS  
 PS Claim 1; Col 19-24; 35pp; English.  
 XX  
 CC This sequence represents the human MDM2 protein. Antibodies that  
 CC specifically bind to human MDM2 protein may be used for detecting  
 CC elevated expression of the MDM2 gene in a human tissue or body fluid  
 CC sample, esp. for cancer diagnosis. The antibodies may be used to  
 CC interfere with the binding of p53 to MDM2. Elevated levels of MDM2 appear  
 CC to sequester p53 and allow the cell to escape from p53-regulated growth.  
 CC (Updated on 25-MAR-2003 to correct PF field.)  
 XX  
 SQ Sequence 491 AA;  
 Query Match 100.0%; Score 553; DB 2; Length 491;  
 Best Local Similarity 100.0%; Pred. No. 7.6e-64;  
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 60  
 DB 17 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76  
 QY 61 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 109  
 DB 77 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 125  
 RESULT 7  
 AAW13380  
 ID AAW13380 standard; protein; 491 AA.  
 XX  
 AC AAW13380;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 05-JUN-1997 (first entry)  
 XX  
 DE Human MDM2 protein.  
 XX  
 KW Human; MDM2; CaCo-2; colonic; carcinoma; probe; detection; amplification;  
 KW elevation; expression; diagnosis; neoplasia; neoplastic transformation;  
 KW sarcoma; colorectal; lung cancer; chronic myelogenous leukaemia.  
 XX  
 OS Homo sapiens.  
 XX

PN US5606044-A.  
 XX  
 PD 25-FEB-1997.  
 XX  
 PF 17-FEB-1995; 95US-00390546.  
 XX  
 PR 07-APR-1992; 92US-00867840.  
 PR 23-JUN-1992; 92US-00903103.  
 PR 07-APR-1993; 93US-00044619.  
 XX  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 PI Kinzler KW, Vogelstein B, Hill DE, Burrell M;  
 XX  
 DR WPI; 1997-153623/14.  
 DR N-PSDB; AAT62065.  
 XX  
 PT Detection of amplification of human MDM2 gene - useful for diagnosis of  
 PT neoplasia or potential neoplastic transformation.  
 XX  
 PS Example 1; Col 21-24; 35pp; English.  
 XX  
 CC The present sequence is the human MDM2 protein, the cDNA for which was  
 CC isolated from a human CaCo-2 colonic carcinoma cell cDNA library using a  
 CC murine MDM2 cDNA probe. The MDM2 cDNA can be used as a probe to detect  
 CC the amplification or elevated expression of a human MDM2 gene, which is  
 CC diagnostic of neoplasia or the potential for neoplastic transformation,  
 CC useful for the detection of, e.g. sarcomas, colorectal carcinoma, lung  
 CC cancer and chronic myelogenous leukaemia. (Updated on 25-MAR-2003 to  
 CC correct PF field.)  
 XX  
 SQ Sequence 491 AA;  
 Query Match 100.0%; Score 553; DB 2; Length 491;  
 Best Local Similarity 100.0%; Pred. No. 7.6e-64;  
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 60  
 DB 17 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76  
 QY 61 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 109  
 DB 77 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 125  
 RESULT 8  
 AAW13600  
 ID AAW13600 standard; protein; 491 AA.  
 XX  
 AC AAW13600;  
 XX  
 DT 16-JAN-1998 (first entry)  
 XX  
 DE Murine double minute 2 protein sequence.  
 XX  
 KW Mouse; Mdm2; murine double minute; phosphoprotein; binding; modulation;  
 KW tumour suppressor; p53; oncogene; cell cycle arrest; p107; antagonist;  
 KW inhibition; transcription factor; adenocarcinoma; colon; cancer; breast;  
 KW lung; stomach; myeloid leukaemia; lymphoma; hyperproliferative;  
 KW restenosis.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO9709343-A2.  
 XX  
 PD 13-MAR-1997.  
 XX  
 PF 02-SEP-1996; 96WO-FR001340.  
 XX  
 PR 04-SEP-1995; 95FR-00010331.  
 XX  
 PA (RHON ) RHONE POULENC RORER SA.



[illegible]

CC acids 1-50 of p53 (see AAW57240); (2) the polypeptide comprises amino  
CC acids 13-41 of p53 (see AAW57240) and at least none additional p53  
CC residues on the N- or C-terminal side, provided that the polypeptide  
CC lacks the homooligomerisation domain of p53; (3) the polypeptide  
CC comprises amino acids 13-41 of p53 (see AAW57241) and at least nine  
CC additional p53 residues on the N- or C-terminal side, provided that the  
CC polypeptide lacks amino acids 138-393 of p53. Some malignant fibrous  
CC histiocytomas and liposarcomas have an MDM2 gene amplification, so  
CC detection of increased expression of MDM2 gene products indicates  
CC tumorigenesis  
XX  
SQ Sequence 491 AA;

Query Match 100.0%; Score 553; DB 2; Length 491;  
Best Local Similarity 100.0%; Pred. No. 7.6e-64;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SQIPASEQETLVPRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQHHIVY 60  
DB 17 SQIPASEQETLVPRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQHHIVY 76  
  
QY 61 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVVNQOESSDSGTSVSEN 109  
DB 77 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVVNQOESSDSGTSVSEN 125

RESULT 11  
AAW42879  
ID AAW42879 standard; protein; 491 AA.  
XX  
AC AAW42879;  
XX  
DT 30-APR-1998 (first entry)  
XX  
DE Amino acid sequence of human MDM2.  
XX  
KW MDM2; tumour; diagnosis; neoplasia; DNA binding protein; p53 polypeptide;  
KW binding; tumour cell; p53-regulated growth; inhibition;  
KW anti-cancer agent.  
XX  
OS Homo sapiens.  
XX  
PN US5708136-A.  
XX  
PD 13-JAN-1998.  
XX  
PF 17-FEB-1995; 95US-00390516.  
XX  
PR 07-APR-1992; 92US-00867840.  
PR 23-JUN-1992; 92US-00903103.  
PR 07-APR-1993; 93US-00044619.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Vogelstein B, Kinzler KW, Burrell M, Hill DE;  
XX  
DR WPI; 1998-100408/09.

XX Human MDM2 binding polypeptide - comprises fragments of p53, useful in re  
XX -establishing p53-regulated growth control in cells over-expressing MDM2.  
XX  
XX Disclosure; Col 23-28; 41pp; English.

XX The present sequence represents human MDM2. The MDM2 gene is amplified in  
XX some human tumours. The amplification of this gene is diagnostic of  
XX neoplasia or its potential. It is speculated that the MDM2 protein is a  
XX potential DNA binding protein that functions in the modulation of  
XX expression of other genes and, when present in excess, interferes with  
XX normal constraints on cell growth. A cell containing three recombinant  
XX DNA constructs was produced. These constructs encode an MDM2 protein  
XX fused to a sequence-specific DNA binding domain, a p53 polypeptide fused  
XX to a transcriptional activation domain, and a reporter gene downstream  
XX from a DNA element which is recognised by the sequence-specific DNA-

CC binding domain. The cell is used to identify a compound which interferes  
CC with the binding of MDM2 and p53. Since MDM2 is overexpressed in tumour  
CC cells and since binding of MDM2 to p53 appears to allow tumour cells to  
CC escape from p53-regulated growth, compounds that inhibit such binding  
CC would be useful as anti-cancer agents

SQ Sequence 491 AA;

Query Match 100.0%; Score 553; DB 2; Length 491;  
Best Local Similarity 100.0%; Pred. No. 7.6e-64;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SQIPASEQETLVPRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQHHIVY 60  
DB 17 SQIPASEQETLVPRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQHHIVY 76  
  
QY 61 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVVNQOESSDSGTSVSEN 109  
DB 77 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVVNQOESSDSGTSVSEN 125

RESULT 12  
AAW42971  
ID AAW42971 standard; protein; 491 AA.  
XX  
AC AAW42971;  
XX  
DT 29-APR-1998 (first entry)  
XX  
DE Amino acid sequence of human MDM2.  
XX  
KW MDM2; tumour; diagnosis; neoplasia; DNA binding protein; p53 polypeptide;  
KW binding; tumour cell; p53-regulated growth; inhibition;  
KW anti-cancer agent.  
XX  
OS Homo sapiens.  
XX  
PN US5702903-A.  
XX  
PD 30-DEC-1997.  
XX  
PF 13-NOV-1995; 95US-00557393.  
XX  
PR 07-APR-1992; 92US-00867840.  
PR 23-JUN-1992; 92US-00903103.  
PR 07-APR-1993; 93US-00044619.  
PR 18-MAY-1994; 94US-00245500.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Vogelstein B, Kinzler KW;  
XX  
DR WPI; 1998-076411/07.  
XX  
N-PSDB; AAV03607.

XX Cell containing reporter construct containing human MDM2 and p53 genes -  
XX for identifying compounds that interfere with binding of human MDM2 to  
XX human p53, useful as anti-cancer agents.  
XX  
XX Disclosure; Coulms 22-28; 37pp; English.  
XX The present sequence represents human MDM2. The MDM2 gene is amplified in  
XX some human tumours. The amplification of this gene is diagnostic of  
XX neoplasia or its potential. It is speculated that the MDM2 protein is a  
XX potential DNA binding protein that functions in the modulation of  
XX expression of other genes and, when present in excess, interferes with  
XX normal constraints on cell growth. A cell containing three recombinant  
XX DNA constructs was produced. These constructs encode an MDM2 protein  
XX fused to a sequence-specific DNA binding domain, a p53 polypeptide fused  
XX to a transcriptional activation domain, and a reporter gene downstream  
XX from a DNA element which is recognised by the sequence-specific DNA-  
XX binding domain. The cell is used to identify a compound which interferes  
XX with the binding of MDM2 and p53. Since MDM2 is overexpressed in tumour

CC cells and since binding of MDM2 to p53 appears to allow tumour cells to  
 CC escape from p53-regulated growth, compounds that inhibit such binding  
 CC would be useful as anti-cancer agents

SQ Sequence 491 AA;  
 Query Match 100.0%; Score 553; DB 2; Length 491;  
 Best Local Similarity 100.0%; Pred. No. 7.6e-64;  
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 60  
 DB 17 SQIPASQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76  
 QY 61 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVVNQESSDSTSVSEN 109  
 DB 77 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVVNQESSDSTSVSEN 125

RESULT 13  
 ID AAW94304 standard; protein; 491 AA.  
 XX AAW94304;  
 AC AAW94304;  
 DT 13-APR-1999 (first entry)  
 DE Human MDM2.  
 KW Human; MDM2; p53; tumorigenesis; growth regulation; diagnosis;  
 KW malignant fibrous histiocytoma; MFH; liposarcoma.  
 XX Homo sapiens.  
 OS US858976-A.  
 PN 12-JAN-1999.  
 PD 14-FEB-1997; 97US-00801718.  
 PF 07-APR-1992; 92US-00867840.  
 PR 23-JUN-1992; 92US-00903103.  
 PR 17-APR-1993; 93US-00044619.  
 PR 17-FEB-1995; 95US-00390515.  
 XX (UJVO) UNIV JOHNS HOPKINS.  
 PA Kinzler KW, Vogelstein B;  
 PI WPI; 1999-152105/13.  
 DR N-PSDB; AAX03947.  
 XX Inhibiting growth of tumour cells having MDM2 gene amplification - with  
 PT MDM2-binding p53 fragment.

Claim 1; Col 23-28; 41pp; English.  
 The present invention describes: (1) a method for inhibiting the growth  
 of tumour cells which contain a human MDM2 gene amplification, comprising  
 administering to the cells a DNA molecule that expresses a polypeptide  
 consisting of a portion of p53 i.e. amino acids 13-41 of the 64 amino  
 acid sequence given in AAW94303, the polypeptide being capable of binding  
 to human MDM2 (the present sequence); (2) a method as in (1) where the  
 polypeptide lacks the homo-oligomerisation domain of p53; and (3) a  
 method as in (1) where the polypeptide lacks amino acids 138-393 of p53.  
 The method is useful for treating the following tumour types which have a  
 MDM2 gene amplification: M-7 malignant fibrous histiocytoma (MFH), M-20  
 MFH, L-9 liposarcoma, KL7 liposarcoma, KL28 liposarcoma, and OSA-CL MFH  
 liposarcoma, and OSA-CL MFH

SQ Sequence 491 AA;  
 Query Match 100.0%; Score 553; DB 2; Length 491;

Best Local Similarity 100.0%; Pred. No. 7.6e-64;  
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQIPASQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 60  
 DB 17 SQIPASQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76  
 QY 61 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVVNQESSDSTSVSEN 109  
 DB 77 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVVNQESSDSTSVSEN 125

RESULT 14  
 ID AAY96567 standard; protein; 491 AA.  
 XX AAY96567;  
 AC AAY96567;  
 DT 12-SEP-2000 (first entry)  
 DE MDM2 oncoprotein.  
 KW hEST2; telomerase; catalytic subunit; reverse transcriptase; life-span;  
 KW retinoblastoma; p53; tumour suppressor; inhibitor; arteriosclerosis;  
 KW proliferation; immortal; tumour therapy; macular degeneration; activator;  
 KW INK4; MDM2; oncoprotein.  
 XX Homo sapiens.  
 OS WO2000031238-A2.  
 PN 02-JUN-2000.  
 PD 24-NOV-1999; 99WO-US027907.  
 PF 25-NOV-1998; 98US-0109891P.  
 PR 17-FEB-1999; 99US-0120549P.  
 XX (GENE-) GENETICA INC.  
 PA Hannon GJ, Beach DH;  
 PI WPI; 2000-400055/34.  
 DR N-PSDB; AAA29389.

New method for increasing the proliferative capacity of cell lines  
 comprises administering agents reversibly activating telomerase activity  
 and reversibly inactivating Rb/INK4 and/or p53 pathways useful in  
 treating age related diseases.

Claim 5; Page 120; 123pp; English.

The invention concerns methods and reagents for extending the life-span,  
 e.g. the number of mitotic divisions, of a cell. The method relies on  
 activation of a telomerase activity and inhibition of one or both of a  
 retinoblastoma (Rb)/INK4 pathway or a p53 pathway. Phosphorylation of Rb  
 by cyclin-dependent kinases, cdk4 and cdk6, releases the cells into the  
 division cycle. Binding of INK4 family members, e.g. the tumour  
 suppressor p16INK4a, inhibits kinase activity and results in growth  
 arrest. Rb inactivators can selectively and reversibly inactivate an  
 Rb/INK4 pathway, especially an Rb/p16INK4a pathway. The oncoprotein MDM2  
 is a cellular inhibitor of Rb/E2F function and the p53 tumour suppressor  
 can also be used in the methods. Other molecules which can be used  
 include cdk4 or cdk6 mutants. In particular, a cdk4 mutant is one which  
 differs from at one or more of residues K22, R24, H95 and/or D97.  
 Additional constructs include a papilloma virus E7 protein, or other  
 viral oncoprotein which bypasses Rb and/or p53. Antisense constructs of  
 the Rb and p16INK4a genes may also be used. The methods are useful for  
 increasing the proliferative capacity of cells. The cells are  
 subsequently of use in pharmaceutical and cosmetic preparations used to  
 treat conditions related to (premature) ageing, e.g. macular degeneration  
 and arteriosclerosis. The cells can also be used to replace tumour cell  
 lines in vitro and for studies on biochemical and physiological aspects

CC of growth and differentiation. Long lived (immortal) cells could also be  
CC of use in the production of normal or genetically engineered  
CC biotechnology products  
XX Sequence 491 AA;  
SQ

Query Match 100.0%; Score 553; DB 3; Length 491;  
Best Local Similarity 100.0%; Pred. No. 7.6e-64;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 60  
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVVNQOESSDSGTSVSEN 109  
Db 77 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVVNQOESSDSGTSVSEN 125

RESULT 15  
AAB48284  
ID AAB48284 standard; protein; 491 AA.  
XX  
AC AAB48284;  
XX

DT 02-APR-2001 (first entry)  
XX  
DE Human MDM2 protein.  
XX

KW S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; 2F;  
KW CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;  
KW Bad; Bcl-2; tumour; cytostatic.  
XX

OS Homo sapiens.  
XX

FN WO2000075184-A1.  
XX

PD 14-DEC-2000.  
XX

XX 05-JUN-2000; 2000WO-US015449.  
XX

XX 04-JUN-1999; 99US-0137494P.  
XX

XX (UYVA ) UNIV YALE.  
XX

XX Zhang H, Tsvetkov LM, Kondo T;  
XX

XX WPI; 2001-061703/07.  
XX

DR N-ESDB; AAC84596.  
XX

XX Modulating polypeptide levels in a cell, diagnosing and treating tumor,  
XX involves altering levels of proteins such as S-phase kinase associated  
XX proteins 1, 2 and cullin/CDC53 proteins.  
XX

PS Claim 5; Page 93-95; 162pp; English.  
XX

XX The invention relates to methods of altering the polypeptide levels in a  
XX cell, using proteins selected from S-phase kinase associated proteins 1  
XX and 2 (SKP1, SKP2), SKP2-like proteins (2F) and CUL-1 (a member of the  
XX cullin/ CDC53 family of proteins). The method is useful for altering the  
XX level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2  
XX polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for  
XX detecting tumours, and in monitoring tumor treatment in a mammal. Agents  
XX that modulate interactions between SKP and target proteins are useful for  
XX treating tumours  
XX

SQ Sequence 491 AA;

Query Match 100.0%; Score 553; DB 4; Length 491;  
Best Local Similarity 100.0%; Pred. No. 7.6e-64;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 60

Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76  
Qy 61 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVVNQOESSDSGTSVSEN 109  
Db 77 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVVNQOESSDSGTSVSEN 125

Search completed: January 27, 2005, 18:06:15  
Job time : 83.8 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 27, 2005, 17:52:56 ; Search time 19.8 Seconds  
(without alignments)  
529.678 Million cell updates/sec

Title: US-10-822-254-2

Perfect score: 553

Sequence: 1 SQIPASQETLVPRKPLLLK.....NLVVNQESDSDGTSVSEN 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	553	100.0	491	1 S24354	p53-binding protei
2	493.5	89.2	489	2 S15349	mdm2 protein - mou
3	276.5	50.0	489	2 S71955	MDM2-like p53-bind
4	78	14.1	685	1 SXPB74	NAD4-protein ADP-r
5	78	14.1	698	1 S31630	NAD4-protein ADP-r
6	78	14.1	698	1 S31714	NAD4-protein ADP-r
7	76	13.7	967	2 A64710	type III restricti
8	72.5	13.1	565	2 S52682	hypothetical prote
9	72	13.0	969	2 E71810	type III restricti
10	71.5	12.9	514	2 D85069	hypothetical prote
11	70.5	12.7	422	2 T26334	hypothetical prote
12	70.5	12.7	838	2 I45557	eyeless, long form
13	69.5	12.6	339	2 A90395	conserved hypothet
14	69	12.5	181	2 S75415	probable ribosomal
15	68.5	12.4	277	2 A10589	conserved hypothet
16	68.5	12.4	331	2 B44938	flagellar motor sw
17	68.5	12.4	517	2 S32169	hypothetical prote
18	68.5	12.4	709	2 S64213	DNA topoisomerase
19	68	12.3	860	2 S64366	hypothetical prote
20	68	12.3	3092	2 S46009	GTPase-activating
21	67.5	12.2	317	2 F97701	hypothetical prote
22	67.5	12.2	401	2 F90288	hypothetical prote
23	67.5	12.2	467	2 T25848	hypothetical prote
24	67	12.1	206	1 XUBWYC	methylated-DNA-[pr
25	67	12.1	261	2 H71680	exodeoxyribonuclea
26	66.5	12.0	447	2 I64002	sodium-translocati
27	66.5	12.0	826	2 B55363	desmocolin, type
28	66.5	12.0	891	2 S27039	preproteins translo
29	66.5	12.0	896	2 A55363	desmocolin, type

RESULT 1

S24354

P53-binding protein mdm2 - human

N:Alternate names: mdm-2 oncogene; mouse double minute 2 homolog; p53-associated phospho

N:Contains: p53-binding protein mdm2, splice form A

C:Species: Homo sapiens (man)

C:Date: 17-Mar-2000 #sequence revision 17-Mar-2000 #text\_change 17-Mar-2000

C:Accession: S24354; S57338; G02026

R:Oliner, J.D.; Kinzler, K.W.; Meltzer, P.S.; George, D.L.; Vogelstein, B.

Nature 358, 80-83, 1992

A:Title: Amplification of a gene encoding a p53-associated protein in human sarcomas.

A:Reference number: S24354; MUID:92310576; PMID:1614537

A:Accession: S24354

A:Molecule type: mRNA

A:Residues: 1-491 <OLI>

A:Cross-references: EMBL:Z12020; NID:g35211; PIDN:CAA78055.1; PID:g35212

R:Zauberman, A.; Flusberg, D.; Haupt, Y.; Barak, Y.; Oren, M.

Nucleic Acids Res. 23, 2584-2592, 1995

A:Title: A functional p53-responsive intronic promoter is contained within the human mdm

A:Reference number: S57338; MUID:95380270; PMID:7651818

A:Accession: S57338

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-16,'p',18-24 <ZAU>

A:Cross-references: EMBL:U28935; NID:g904033; PIDN:AAA82237.1; PID:g904034

R:Lunec, J.

submitted to the EMBL Data Library, August 1995

A:Description: Multiple alternate spliced mdm2 transcripts with loss of p53 binding doma

A:Reference number: G09070

A:Accession: G02026

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-27,223-491 <LUN>

A:Cross-references: EMBL:U33199; NID:g992676; PIDN:AAA75514.1; PID:g992677

A:Experimental source: splice form A

C:Genetics:

A:Gene: GDB:MDM2

A:Cross-references: GDB:250456; OMIM:164785

A:Map position: l2q14.3-12q15

C:Superfamily: human p53-binding protein mdm2

C:Keywords: alternative splicing; oncogene; phosphoprotein

F:1-491/Product: p53-binding protein mdm-2 #status predicted <MAT1>

F:1-27,223-491/Product: p53-binding protein mdm-2, splice form A #status predicted <MAT2>

Query Match 100.0%; Score 553; DB 1; Length 491;

Best Local Similarity 100.0%; Pred. No. 2.6e-49;

Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASQETLVPRKPLLLKLLKSVGAQKQDTYTMKEVLFYLGQYIMTKRLYDEKQOHLVY 60

Db 17 SQIPASQETLVPRKPLLLKLLKSVGAQKQDTYTMKEVLFYLGQYIMTKRLYDEKQOHLVY 76



[illegible]



	Query Match	12.5%	Score 69	DB 2	Length 181
	Best Local Similarity	24.2%	Pred. No. 7.9		
	Matches 29	Conservative 20	Mismatches 39	Indels 32	Gaps 4
Qy	9	ETLVRPPLLLKLLKSVGAQKDYTMKEVLFLYQGYIMTKRL	----	YDEKQOHIVYCSND	64
Db	65	ERAVREQLVGLKLLKMGLLKKETATVDILSLTBQDLLERLQTIYVKKGLSLNTIYQARQ	----	124	
Qy	65	LL-----GDLFGVPSFSVKEHKIYTMIRNLV-----	----	VVNQOERSSDG	103
Db	125	LIHTGHTAVNGKRYTSPGIYVNDVE-----	----	NLIIDYVTSFSPKRPVMSOEGGBIG	177





AGE BLANK (USPTO)

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 27, 2005, 17:51:46 ; Search time 84.6 Seconds  
(without alignments)  
741.322 Million cell updates/sec

Title: US-10-822-254-2

Perfect score: 553

Sequence: 1 SQIPASQETLVLRPKPLLLK.....NLVVNQESSDGSCTSVSEN 109

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	553	100.0	166	Q8NDW2	Q8ndw2 homo sapien
2	553	100.0	195	Q96DS4	Q96ds4 homo sapien
3	553	100.0	243	Q8TE47	Q8te47 homo sapien
4	553	100.0	491	1 QM22.HUMAN	Q00987 homo sapien
5	553	100.0	491	2 AAP35922	Aap35922 homo sapi
6	553	100.0	491	2 AAH67077	Aah67077 homo sapi
7	541	97.8	487	1 QM22.CANFA	P56950 canis famil
8	541	97.8	487	2 Q9GMZ6	Q9gmz6 canis famil
9	541	97.8	491	1 QM22.HORSE	P56951 equus cabal
10	538	97.3	491	2 Q7YRZ8	Q7yrz8 felis silve
11	503	91.0	436	2 Q8WYJ2	Q8wyj2 homo sapien
12	493.5	89.2	489	1 QM22.MOUSE	P23804 mus musculu
13	493.5	89.2	489	2 Q9LXK7	Q9lxx7 m mus muscu
14	476	86.1	118	2 Q8WYJ3	Q8wyj3 homo sapien
15	469.5	84.9	466	1 QM22.MESAU	Q60524 mesocricetu
16	415	75.0	325	2 Q9PVL2	Q9pvl2 gallus gall
17	407	73.6	173	2 Q8TE46	Q8te46 homo sapien
18	358	64.7	473	1 QM22.XENLA	P56273 xenopus lae
19	358	64.7	473	2 Q6GMBS	Q6gmb5 xenopus lae
20	357	64.6	482	2 Q6P309	Q6p3q9 xenopus tro
21	357	64.6	482	2 AAH63898	Aah63898 xenopus t
22	339	61.3	105	2 Q8NDW0	Q8ndw0 homo sapien
23	320	57.9	426	2 Q8GK41	Q8gk41 canis famil
24	292.5	52.9	445	1 QM22.BRARE	Q42354 brachydanio
25	292.5	52.9	445	2 AA00198	AA00198 brachydanio
26	280.5	50.7	446	2 Q8WYJ1	Q8wyj1 homo sapien
27	276.5	50.0	489	1 QM24.MOUSE	Q35618 mus musculu
28	273.5	49.5	489	2 Q8CYG1	Q8cyg1 m mus muscu
29	268	48.5	491	2 Q7ZUW7	Q7zuw7 brachydanio
30	267	48.3	490	2 Q99L86	Q99l86 mus musculu
31	266	48.1	475	2 Q7ZYI3	Q7zyi3 xenopus lae

32	254.5	46.0	134	2 Q6PHL8	Q6phl8 xenopus lae
33	254.5	46.0	134	2 AAH56503	Aah56503 xenopus l
34	251	45.4	153	2 Q6MZR7	Q6mzr7 homo sapien
35	251	45.4	153	2 CAE45961	Caeh45961 homo sapi
36	251	45.4	490	2 AAH67299	Aah67299 homo sapi
37	249	45.0	490	1 QM24.HUMAN	O15151 homo sapien
38	223	40.3	69	2 Q86WA4	Q86wa4 homo sapien
39	216	39.1	66	2 Q96DS3	Q96ds3 homo sapien
40	213	38.5	70	2 Q86WA3	Q86wa3 homo sapien
41	199	36.0	95	2 Q96DS1	Q96ds1 homo sapien
42	179.5	32.5	70	2 Q8NDW1	Q8ndw1 homo sapien
43	177	32.0	159	2 Q96DS0	Q96ds0 homo sapien
44	176	31.8	60	2 Q96DS5	Q96ds5 homo sapien
45	176	31.8	130	2 Q9H4C3	Q9h4c3 homo sapien

#### ALIGNMENTS

##### RESULT 1

Q8NDW2 ID Q8NDW2 PRELIMINARY; PRT; 166 AA.  
AC Q8NDW2;  
DT 01-OCT-2002 (Tremblrel. 22, Created)  
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)  
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
DE P53-binding protein.  
GN Name=MDM2;  
OS Homo sapiens (Human);  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bartel F., Pinkert D., Kappler M., Bache M., Schmidt H., Taubert H.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ491698; CAD36959.1; -.  
DR HSSP; Q9UNT8; 1YCR.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR InterPro; IPR010984; MDM2.  
DR InterPro; IPR003121; SWIB\_MDM2.  
DR Pfam; PF02201; SWIB; 1.  
SQ SEQUENCE 166 AA; 18900 MW; FA6B5BA18E85040D CRC64;

Query Match 100.0%; Score 553; DB 2; Length 166;  
Best Local Similarity 100.0%; Pred. No. 1.2e-51;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASQETLVLRPKPLLLKLLKSVGAKQOTYTKVELFYLGQYIMTKRLYDEKQOHIVY 60  
Db 17 SQIPASQETLVLRPKPLLLKLLKSVGAKQOTYTKVELFYLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPSPFSVKEHRKIYTMTRYNLVVNQESSDGSCTSVSEN 109  
Db 77 CSNDLLGDLFGVPSPFSVKEHRKIYTMTRYNLVVNQESSDGSCTSVSEN 125

##### RESULT 2

Q96DS4 ID Q96DS4 PRELIMINARY; PRT; 195 AA.  
AC Q96DS4;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
DE MDM2 variant FB26.  
GN Name=MDM2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Rhabdomyosarcoma tumor;

RA Bartel F., Taylor A.C., Taubert H., Harris L.C.;  
 RL Submitted (MAY-2001) to the ENBL/GenBank/DBJ databases.

DR ENBL; AF385323; AAL13243.1; --  
 DR HSSP; Q9UMT8; 1YCR.

DR GO; GO:0005634; C:nucleus; IEA.

DR InterPro; IPR010984; MDM2.

DR InterPro; IPR003121; SWIB\_MDM2.

DR Pfam; PF02201; SWIB; 1.

SQ SEQUENCE 195 AA; 22161 MW; 4987AE567DB12D5D CRC64;

Query Match 100.0%; Score 553; DB 2; Length 195;

Best Local Similarity 100.0%; Pred. No. 1.4e-51;

Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASQETLVRPKPLLLKLLKSVGAQKDYTMKEVLFLYGQYIMTKRLYDEKQHIIVY 60

Db 17 SQIPASQETLVRPKPLLLKLLKSVGAQKDYTMKEVLFLYGQYIMTKRLYDEKQHIIVY 76

Qy 61 CSNDLLGLDFGVPSFVKEHRKIYTMIRNLVNVNQESSDGSSTSVSEN 109

Db 77 CSNDLLGLDFGVPSFVKEHRKIYTMIRNLVNVNQESSDGSSTSVSEN 125

RESULT 3

Q8TE47 PRELIMINARY; PRT; 243 AA.

Q8TE47

DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE MDM2 isoform KB9 protein.

GN Name=MDM2 isoform KB9;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM MDM2).

RC TISSUE=Lymphocytes;

RA Bartel F., Pinkert D., Kappler M., Bache M., Schmidt H., Taubert H.;

RL Submitted (FEB-2002) to the ENBL/GenBank/DBJ databases.

DR ENBL; AJ430612; CAD23251.1; --

DR HSSP; Q9UMT8; 1YCR.

DR GO; GO:0005634; C:nucleus; IEA.

DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.

DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.

DR GO; GO:0008270; F:zinc ion binding; IEA.

DR GO; GO:0016567; P:protein ubiquitination; IEA.

DR InterPro; IPR010984; MDM2.

DR InterPro; IPR003121; SWIB\_MDM2.

DR InterPro; IPR001841; Znf\_Fing.

DR Pfam; PF02201; SWIB; 1.

DR SMART; SM00184; RING; 1.

DR PROSITE; PS00089; ZF\_RING\_2; 1.

SQ SEQUENCE 243 AA; 27317 MW; 9EB5D0142CF185A2 CRC64;

Query Match

Best Local Similarity 100.0%; Score 553; DB 2; Length 243;

Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASQETLVRPKPLLLKLLKSVGAQKDYTMKEVLFLYGQYIMTKRLYDEKQHIIVY 60

Db 17 SQIPASQETLVRPKPLLLKLLKSVGAQKDYTMKEVLFLYGQYIMTKRLYDEKQHIIVY 76

Qy 61 CSNDLLGLDFGVPSFVKEHRKIYTMIRNLVNVNQESSDGSSTSVSEN 109

Db 77 CSNDLLGLDFGVPSFVKEHRKIYTMIRNLVNVNQESSDGSSTSVSEN 125

RESULT 4

MDM2\_HUMAN

ID\_MDM2\_HUMAN STANDARD; PRT; 491 AA.

AC Q00987; Q13226; Q13297; Q13298; Q13299; Q13300; Q13301; Q9UGI3;

Q9UMT8;

01-APR-1993 (Rel. 25, Created)

01-APR-1993 (Rel. 25, Last sequence update)

01-OCT-2004 (Rel. 45, Last annotation update)

Ubiqutin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein

MDM2) (Oncoprotein Mdm2) (Double minute 2 protein) (hdm2).

GN Name=MDM2;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM MDM2).

RC MEDLINE=923110576; PubMed=1614537;

RA Oliner J.D., Kinzler K.W., Meltzer P.S., George D.L., Vogelstein B.;

"Amplification of a gene encoding a p53-associated protein in human

sarcomas.";

RL Nature 358:80-83(1992).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORMS MDM2-A; -B; -C; -D AND -E).

RC TISSUE=Ovarian carcinoma;

RA Sigalas I., Calvert A.H., Anderson J.J., Neal D.E., Lunec J.;

"Alternatively spliced mdm2 transcripts with loss of p53 binding

domain sequences: transforming ability and frequent detection in human

cancer.";

RL Nat. Med. 2:912-917(1996).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM MDM2-ALPHA).

RC MEDLINE=20065171; PubMed=10597303;

RA Velthoen N., Metcalfe S., Milner J.;

"A novel exon within the mdm2 gene modulates translation initiation in

vitro and disrupts the p53-binding domain of mdm2 protein.";

RL Oncogene 18:7026-7033(1999).

RN [4]

RP SEQUENCE FROM N.A. (ISOFORM MDM2).

RC Rieder M.J., Livingston R.J., Braun A.C., Montoya M.A., Chung M.-W.,

Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,

Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;

"NIHES-SNPs, environmental genome project, NIHES ES15478, Department

of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";

RL Submitted (JUL-2002) to the ENBL/GenBank/DBJ databases.

RN [5]

RP SEQUENCE FROM N.A. (ISOFORM MDM2).

RC TISSUE=Muscle;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

Whitting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Trinchero J., Schmutz J., Myers R.M.,

Butterfield V.S.N., Krzywinski M.I., Skalska U., Smal M.A.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [6]

RP SEQUENCE OF 6-491 FROM N.A. (ISOFORM MDM2-A1).

RA Liang H., Atkins H., Abdel-Fattah R., Saeyun R., Lunec J.;

"Genomic organisation of the human MDM2 oncogene and relationship to

its alternatively spliced mRNA's";

RL Submitted (NOV-1999) to the ENBL/GenBank/DBJ databases.

RN [7]

RP SEQUENCE OF 1-24 FROM N.A.  
 RX MEDLINE=93380270; PubMed=7651818;  
 RA Zauberman A., Flusberg D., Haupt Y., Barak Y., Oren M.;  
 RT "A functional p53-responsive intronic promoter is contained within the  
 RT human mdm2 gene.";  
 RL Nucleic Acids Res. 23:2584-2592(1995).  
 RN [8]  
 RP SEQUENCE OF 1-9 FROM N.A.  
 RX MEDLINE=97413643; PubMed=9270029;  
 RA Landers J.E., Cassel S.L., George D.L.;  
 RT "Translational enhancement of mdm2 oncogene expression in human tumor  
 RT cells containing a stabilized wild-type p53 protein.";  
 RL Cancer Res. 57:3562-3568(1997).  
 RN [9]  
 RP SEQUENCE OF 301-481 FROM N.A.  
 RX MEDLINE=20542019; PubMed=11087894;  
 RA Taubert H., Kappler M., Meyer A., Bartel P., Schlott T.,  
 RA Lautenschlaeger C., Bache M., Schmidt H., Wuerl P.;  
 RT "A MboII polymorphism in exon 11 of the human MDM2 gene occurring in  
 RT normal blood donors and in soft tissue sarcoma patients: an indication  
 RT for an increased cancer susceptibility?";  
 RL Mutat. Res. 456:39-44(2000).  
 RN [10]  
 RP MUTAGENESIS OF CVS-464.  
 RX MEDLINE=98111004; PubMed=9450543;  
 RA Honda R., Tanaka H., Yasuda H.;  
 RT "Oncoprotein MDM2 is a ubiquitin ligase E3 for tumor suppressor p53.";  
 RL FEBS Lett. 420:25-27(1997).  
 RN [11]  
 RP MUTAGENESIS OF CVS-449.  
 RX MEDLINE=20190101; PubMed=10723139;  
 RA Honda R., Yasuda H.;  
 RT "Activity of MDM2, a ubiquitin ligase, toward p53 or itself is  
 RT dependent on the RING finger domain of the ligase.";  
 RL Oncogene 19:1473-1476(2000).  
 RN [12]  
 RP MUTAGENESIS.  
 RX MEDLINE=20187618; PubMed=10727242;  
 RA Fang S., Jensen J.P., Ludwig R.L., Vousden K.H., Weissman A.M.;  
 RT "Mdm2 is a RING finger-dependent ubiquitin protein ligase for itself  
 RT and p53.";  
 RL J. Biol. Chem. 275:8945-8951(2000).  
 RN [13]  
 RP MUTAGENESIS OF CVS-441 AND CVS-478.  
 RX MEDLINE=20076498; PubMed=10608892;  
 RA Sharp D.A., Kratowicz S.A., Sank M.J., George D.L.;  
 RT "Stabilization of the MDM2 oncoprotein by interaction with the  
 RT structurally related MDMX protein.";  
 RL J. Biol. Chem. 274:38189-38196(1999).  
 RN [14]  
 RP NUCLEOLAR LOCALIZATION SIGNAL.  
 RX MEDLINE=20173879; PubMed=10707090;  
 RA Lohrum M.A.E., Ahecroft M., Kubbutat M.H.G., Vousden K.H.;  
 RT "Identification of a cryptic nucleolar-localization signal in MDM2.";  
 RL Nat. Cell Biol. 2:179-181(2000).  
 RN [15]  
 RP PHOSPHORYLATION BY ATM.  
 RX MEDLINE=20079591; PubMed=10611322;  
 RA Khosravi R., Maya R., Gottlieb T., Oren M., Shiloh Y., Shkedy D.;  
 RT "Rapid ATM-dependent phosphorylation of MDM2 precedes p53 accumulation  
 RT in response to DNA damage.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 96:14973-14977(1999).  
 RN [16]  
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 25-109 IN COMPLEX WITH P53.  
 RX MEDLINE=97081050; PubMed=8875929;  
 RA Kussie P.H., Gorina S., Marechal V., Elenbaas B., Moreau J.,  
 RA Levine A.J., Pavletich N.P.;  
 RT "Structure of the MDM2 oncoprotein bound to the p53 tumor suppressor  
 RT transactivation domain.";  
 RL Science 274:948-953(1996).  
 CC -1- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and  
 CC apoptosis by binding its transcriptional activation domain.  
 CC Functions as a ubiquitin ligase E3, in the presence of E1 and E2,

CC toward p53 and itself. Permits the nuclear export of p53 and  
 CC targets it for proteasome-mediated proteolysis.  
 CC -1- COFACTOR: Zinc is required for ubiquitin ligase E3 activity.  
 CC -1- SUBUNIT: Binds p53, p73, ARF(p14), ribosomal protein L5 and  
 CC specifically to RNA. Can interact also with retinoblastoma protein  
 CC (RB). E1A-associated protein EP300 and the E2F1 transcription  
 CC factor.  
 CC -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed  
 CC predominantly in the nucleoplasm. Interaction with ARF(p14)  
 CC results in the localization of both proteins to the nucleolus. The  
 CC nucleolar localization signals in both ARF(p14) and MDM2 may be  
 CC necessary to allow efficient nucleolar localization of both  
 CC proteins.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=8;  
 CC Name=Mdm2;  
 CC IsoId=Q00987-1; Sequence=Displayed;  
 CC Name=Mdm2-A;  
 CC IsoId=Q00987-2; Sequence=VSP\_003208;  
 CC Name=Mdm2-A1;  
 CC IsoId=Q00987-3; Sequence=VSP\_003208, VSP\_003214;  
 CC Name=Mdm2-B;  
 CC IsoId=Q00987-4; Sequence=VSP\_003209;  
 CC Name=Mdm2-C;  
 CC IsoId=Q00987-5; Sequence=VSP\_003211;  
 CC Name=Mdm2-D;  
 CC IsoId=Q00987-6; Sequence=VSP\_003210;  
 CC Name=Mdm2-E;  
 CC IsoId=Q00987-7; Sequence=VSP\_003212, VSP\_003213;  
 CC Name=Mdm2-alpha;  
 CC IsoId=Q00987-8; Sequence=VSP\_003207;  
 CC -1- TISSUE SPECIFICITY: Ubiquitous. Isoforms MDM2-A, -B, -C, -D and -E  
 CC are observed in a range of human cancers but absent in normal  
 CC tissues.  
 CC -1- INDUCTION: By DNA damage.  
 CC -1- DOMAIN: Region I is sufficient for binding p53 and inhibiting its  
 CC G1 arrest and apoptosis functions. It also binds p73 and E2F1.  
 CC Region II contains most of a central acidic region required for  
 CC interaction with ribosomal protein L5 and a putative C4-type zinc  
 CC finger. The RING finger domain which coordinates two molecules of  
 CC zinc interacts specifically with RNA whether or not zinc is  
 CC present and mediates the hetero-oligomerization with MDM4. It is  
 CC also essential for its ubiquitin ligase E3 activity toward p53 and  
 CC itself.  
 CC -1- PTM: Phosphorylated in response to ionizing radiation in an ATM-  
 CC dependent manner.  
 CC -1- DISEASE: Seems to be amplified in certain tumors (including soft  
 CC tissue sarcomas, osteosarcomas and gliomas). A higher frequency of  
 CC splice variants lacking p53 binding domain sequences was found in  
 CC late-stage and high-grade ovarian and bladder carcinomas. Four of  
 CC the splice variants show loss of p53 binding.  
 CC -1- MISCELLANEOUS: MDM2 RING finger mutations that failed to  
 CC Query Match 100.0%; Score 553; DB 1; Length 491;  
 CC Best Local Similarity 100.0%; Pred. No. 4e-51;  
 CC Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 SQIPASQETLVVRPKPLLLKLLKSVGAKQTYTWMKEVLFLYGQVIMTKRLYDEKQOHIVY 60  
 Db 17 SQIPASQETLVVRPKPLLLKLLKSVGAKQTYTWMKEVLFLYGQVIMTKRLYDEKQOHIVY 76  
 Qy 61 CSNDLLGDLFGVPSFVKHKKIYTMIVRYLVVNVNQESSDGSSTSVSN 109  
 Db 77 CSNDLLGDLFGVPSFVKHKKIYTMIVRYLVVNVNQESSDGSSTSVSN 125  
 RESULT 5  
 AAP35922  
 ID AAP35922 PRELIMINARY; PRT; 491 AA.  
 AC AAP35922  
 DT 02-MAR-2004 (Tremblrel. 27, Created)  
 DT 02-MAR-2004 (Tremblrel. 27, Last sequence update)  
 DT 02-MAR-2004 (Tremblrel. 27, Last annotation update)

Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (Mouse).

DE Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC NCBI\_TaxID=9606;

CC [1]

CC SEQUENCE FROM N.A.

RA Kainine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S., Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y., Phelan M., Farmer A.;

RA "Cloning of human full-length CDSs in BD Creator(TM) System Donor vector.";

RT Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.

RL EMBL; BT007258; AAP35922.1; -- F37CE163876BC983 CRC64;

DR EMBL; BT007258; AAP35922.1; -- F37CE163876BC983 CRC64;

SQ SEQUENCE 491 AA; 55232 MW; F37CE163876BC983 CRC64;

Query Match 100.0%; Score 553; DB 2; Length 491;

Best Local Similarity 100.0%; Pred. No. 4e-51;

Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SQIPASQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQHIVY 60

Db 17 SQIPASQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQHIVY 76

Oy 61 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 109

Db 77 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 125

RESULT 7

ID MDM2 CANFA STANDARD; PRT; 487 AA.

AC P56950; Q95KN5;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Cdm2).

GN Name=MDM2;

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OC NCBI\_TaxID=9615;

CC [1]

CC SEQUENCE OF 1-484 FROM N.A.

RP MEDLINE=20218866; PubMed=10754200;

RA Nasir L., Burr P.D., McFarlane S.T., Gault E., Thompson H., Argyle D.J.;

RT "Cloning, sequence analysis and expression of the cDNAs encoding the canine and equine homologues of the mouse double minute 2 (mdm2) proto-oncogene.";

RT Cancer Lett. 152:9-13 (2000).

CC [2]

CC SEQUENCE FROM N.A. (ISOFORMS MDM2 AND MDM2-ALPHA).

RA MEDLINE=20065171; PubMed=10597303;

RA Velthoen N., Metcalfe S., Milner J.;

RT "A novel exon within the mdm2 gene modulates translation initiation in vitro and disrupts the p53-binding domain of mdm2 protein.";

RL Oncogene 18:7026-7033 (1999).

CC -1- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and apoptosis by binding its transcriptional activation domain. Functions as a ubiquitin ligase E3, in the presence of E1 and E2, toward p53 and itself. Permits the nuclear export of p53 and targets it for proteasome-mediated proteolysis (By similarity).

CC -1- COPACTOR: Zinc is required for ubiquitin ligase E3 activity (By similarity).

CC -1- SUBUNIT: Binds p53, p73, ARF(p14), ribosomal protein L5 and specifically to RNA. Can interact also with retinoblastoma protein (RB), E1A-associated protein E1A and the E2F1 transcription factor (By similarity).

CC -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed predominantly in the nucleoplasm (By similarity).

CC -1- ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=2; Name=Mdm2; IsoId=P56950-1; Sequence=Displayed;

CC Name=Mdm2-alpha; IsoId=P56950-2; Sequence=VSP 003206;

CC -1- TISSUE SPECIFICITY: Isoform Mdm2-alpha is present in lymphoid and testicular tissues.

CC -1- DOMAIN: Region I is sufficient for binding p53 and inhibiting its G1 arrest and apoptosis functions. It also binds p73 and E2F1. Region II contains most of a central acidic region required for interaction with ribosomal protein L5 and a putative C4-type zinc finger. The RING finger domain which coordinates two molecules of zinc interacts specifically with RNA whether or not zinc is present and mediates the hetero-oligomerization with MDM4. It is

Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (Mouse).

DE Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC NCBI\_TaxID=9606;

CC [1]

CC SEQUENCE FROM N.A.

RA Kainine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S., Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y., Phelan M., Farmer A.;

RA "Cloning of human full-length CDSs in BD Creator(TM) System Donor vector.";

RT Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.

RL EMBL; BT007258; AAP35922.1; -- F37CE163876BC983 CRC64;

DR EMBL; BT007258; AAP35922.1; -- F37CE163876BC983 CRC64;

SQ SEQUENCE 491 AA; 55232 MW; F37CE163876BC983 CRC64;

Query Match 100.0%; Score 553; DB 2; Length 491;

Best Local Similarity 100.0%; Pred. No. 4e-51;

Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SQIPASQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQHIVY 60

Db 17 SQIPASQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQHIVY 76

Oy 61 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 109

Db 77 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 125

RESULT 6

AAH67077 PRELIMINARY; PRT; 491 AA.

AC AAH67077;

DT 14-APR-2004 (TrEMBLrel. 27, Created)

DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)

DT 14-APR-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC NCBI\_TaxID=9606;

CC [1]

CC SEQUENCE FROM N.A.

RC TISSUE=Muscle;

RA MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C., Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S.G., Garcia A.M., Gay L.J., Hulyk S.W., Villaton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanches A., Blakesley R.W., Touchman A.C., Shevchenko Y., Bouffard G.G., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;

RA "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

CC [2]

CC SEQUENCE FROM N.A.

RC TISSUE=Muscle;

RA Strausberg R.;

RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC067077; AAH67077.1; --

KW Hypothetical protein.

CC also essential for its ubiquitin ligase E3 activity toward p53 and  
 CC itself (By similarity).  
 CC -!- SIMILARITY: Belongs to the MDM2 / MDM4 family.  
 CC -!- SIMILARITY: Contains 1 RanBP2-type zinc finger.  
 CC -!- SIMILARITY: Contains 1 RING-type zinc finger.  
 CC -!- SIMILARITY: Contains 1 SWIB domain.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).  
 CC -----  
 CC EMBL; AF100705; AAF67833.1; -;  
 CC EMBL; AF322416; AAG42840.1; -;  
 CC HSSP; Q9UMT8; 1YCR.  
 CC InterPro; IPR0010984; MDM2.  
 CC InterPro; IPR003121; SWIB.  
 CC InterPro; IPR001876; Znf RangDP.  
 CC InterPro; IPR001841; Znf\_ring.  
 CC Pfam; PF02201; SWIB; 1.  
 CC Pfam; PF00641; zf-RanBP; 1.  
 CC SMART; SM00184; RING; 1.  
 CC PROSITE; PS01358; ZF\_RANBP2\_1; 1.  
 CC PROSITE; PS01199; ZF\_RANBP2\_2; 1.  
 CC PROSITE; PS00518; ZF\_RING\_1; FALSE\_NEG.  
 CC PROSITE; PS00089; ZF\_RING\_2; 1.  
 CC Alternative splicing; Ligase; Metal-binding; Nuclear protein;  
 KW Ub1 conjugation pathway; Zinc; Zinc-finger.  
 FT DOMAIN 27 107 SWIB.  
 FT DOMAIN 179 185 Nuclear localization signal (Potential).  
 FT DOMAIN 190 202 Nuclear export signal.  
 FT DOMAIN 210 304 ARF-binding.  
 FT DOMAIN 210 215 Poly-Ser.  
 FT DOMAIN 242 331 Region II.  
 FT DOMAIN 243 301 Asp/Glu-rich (acidic).  
 FT ZN\_FING 299 328 RanBP2-type.  
 FT ZN\_FING 434 475 RING-type.  
 FT DOMAIN 462 469 Nucleolar localization signal  
 FT VARSPLIC 1 61 Missing (in isoform Mdm2-alpha).  
 FT CONFLICT 11 11 /FTID=VSP\_003206.  
 FT CONFLICT 238 239 G -> D (in Ref. 2).  
 FT CONFLICT 239 239 OD -> HH (in Ref. 2).  
 SQ SEQUENCE 487 AA; 54696 MW; 60CDB470A32A8E69 CRC64;  
 Query Match 97.8%; Score 541; DB 1; Length 487;  
 Best Local Similarity 97.2%; Pred. No. 7.9e-50;  
 Matches 106; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTKKEVLFYLGQYIMTKRLYDEKQOHIVY 60  
 DB 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTKKEVLFYLGQYIMTKRLYDEKQOHIVY 76  
 QY 61 CSNDLLGLDFGVPSFVKHEHKIYTMIRNLVNVNQSSDSGTSVSEN 109  
 DB 77 CSNDLLGLDFGVPSFVKHEHKIYTMIRNLVNVNQHEPSPSGTSVSEN 125  
 RESULT 8  
 ID Q9GMZ6 PRELIMINARY; PRT; 487 AA.  
 AC Q9GMZ6  
 DT 01-MAR-2001 (TRENBLrel. 16, Created)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
 DE MDM2.  
 GN Name=mdm2;  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA Setouchi A., Tsujimoto H.;  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB031276; BAB11975.1; -;  
 DR HSSP; Q9UMT8; 1YCR.  
 DR GO; GO:0005730; C:nucleolus; ISS.  
 DR GO; GO:0005654; C:nucleoplasm; ISS.  
 DR GO; GO:0017163; F:negative regulator of basal transcription a. . .; ISS.  
 DR GO; GO:0005515; F:protein binding; ISS.  
 DR GO; GO:0000122; P:negative regulation of transcription from P. . .; ISS.  
 DR InterPro; IPR0010984; MDM2.  
 DR InterPro; IPR003121; SWIB MDM2.  
 DR InterPro; IPR001876; Znf RangDP.  
 DR InterPro; IPR001841; Znf\_ring.  
 DR Pfam; PF02201; SWIB; 1.  
 DR Pfam; PF00641; zf-RanBP; 1.  
 DR SMART; SM00184; RING; 1.  
 DR PROSITE; PS01358; ZF\_RANBP2\_1; 1.  
 DR PROSITE; PS01199; ZF\_RANBP2\_2; 1.  
 DR PROSITE; PS00089; ZF\_RING\_2; 1.  
 SQ SEQUENCE 487 AA; 54724 MW; 34FC5CC6A18D7744 CRC64;  
 Query Match 97.8%; Score 541; DB 2; Length 487;  
 Best Local Similarity 97.2%; Pred. No. 7.9e-50;  
 Matches 106; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTKKEVLFYLGQYIMTKRLYDEKQOHIVY 60  
 DB 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTKKEVLFYLGQYIMTKRLYDEKQOHIVY 76  
 QY 61 CSNDLLGLDFGVPSFVKHEHKIYTMIRNLVNVNQSSDSGTSVSEN 109  
 DB 77 CSNDLLGLDFGVPSFVKHEHKIYTMIRNLVNVNQHEPSPSGTSVSEN 125  
 RESULT 9  
 ID MDM2\_HORSE STANDARD; PRT; 491 AA.  
 AC P56951;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein  
 DE Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Bdm2).  
 GN Name=MDM2;  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20219866; PubMed=10754200;  
 RA Nasir L., Burr P.D., McFarlane S.T., Gault E., Thompson H.,  
 RA Argyle D.J.;  
 RT "Cloning, sequence analysis and expression of the cDNAs encoding the  
 RT canine and equine homologues of the mouse double minute 2 (mdm2)  
 RT proto-oncogene.";  
 RL Cancer Lett. 152:9-13 (2000).  
 CC -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and  
 CC apoptosis by binding its transcriptional activation domain.  
 CC Functions as a ubiquitin ligase E3, in the presence of E1 and E2,  
 CC toward p53 and itself. Promotes the nuclear export of p53 and  
 CC targets it for proteasome-mediated proteolysis (By similarity).  
 CC -!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity (By  
 CC similarity).  
 CC -!- SUBUNIT: Binds p53, p73, ARF(p14), ribosomal protein L5 and  
 CC specifically to RNA. Can interact also with retinoblastoma protein  
 CC (RB), E1a-associated protein EP300 and the E2F1 transcription  
 CC factor (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed

CC predominantly in the nucleoplasm (By similarity).

CC -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its

CC G1 arrest and apoptosis functions. It also binds p73 and E2F1.

CC Region II contains most of a central acidic region required for

CC interaction with ribosomal protein L5 and a putative C4-type zinc

CC finger. The RING finger domain which coordinates two molecules of

CC zinc interacts specifically with RNA whether or not zinc is

CC present and mediates the hetero-oligomerization with MDM4. It is

CC also essential for its ubiquitin ligase E3 activity toward p53 and

CC itself (By similarity).

CC -!- SIMILARITY: Belongs to the MDM2 / MDM4 family.

CC -!- SIMILARITY: Contains 1 RANBP2-type zinc finger.

CC -!- SIMILARITY: Contains 1 RING-type zinc finger.

CC -!- SIMILARITY: Contains 1 SWIB domain.

CC -----

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----

CC EMBL: AF121140; AAF28866.1; -

CC HSP; Q9UMT8; 1YCR

CC InterPro: IPR010984; MDM2.

CC InterPro: IPR003121; SWIB.

CC InterPro: IPR001876; Znf\_RanGDP.

CC InterPro: IPR001841; Znf\_Ring.

CC Pfam: PF02201; SWIB; 1.

CC Pfam: PF00641; zf-RanBP; 1.

CC SMART; SM00184; RING; 1.

CC PROSITE; PS01358; ZF\_RANBP2\_1; 1.

CC PROSITE; PS01199; ZF\_RANBP2\_2; 1.

CC PROSITE; PS00518; ZF\_RING\_1; FALSE\_NEG.

CC PROSITE; PS00089; ZF\_RING\_2; 1.

CC LIGase; Metal-binding; NuClear protein; Ubl conjugation pathway; Zinc;

CC Zinc-finger.

CC FT DOMAIN 27 107 SWIB.

CC FT DOMAIN 179 185 Nuclear localization signal (Potential).

CC FT DOMAIN 190 202 Nuclear export signal.

CC FT DOMAIN 210 304 ARF-binding.

CC FT DOMAIN 210 215 Poly-Ser.

CC FT DOMAIN 242 331 Region II.

CC FT DOMAIN 243 301 Asp/Glu-rich (acidic).

CC FT ZN FING 299 328 RANBP2-type.

CC FT ZN FING 438 479 RING-type.

CC FT DOMAIN 466 473 Nuclear localization signal (Potential).

CC SEQUENCE 491 AA; 55279 MW; 641E033D5C1DEC39 CRC64;

Query Match 97.8%; Score 541; DB 1; Length 491;

Best Local Similarity 97.2%; Pred. No. 8e-50;

Matches 106; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SQPASEQETLVRPKLLKLLKSVGAQKDTYTMKEVFLVGLGYIMTKRLYDEKQHHIVY 60

DB 17 SQPASEQETLVRPKLLKLLKSVGAQKDTYTMKEVFLVGLGYIMTKRLYDEKQHHIVY 76

QY 61 CSNDLLGLDGLFGVPSFVSKEHKIYTMIRNLVNVNQESDSDGTSVSEN 109

DB 77 CSNDLLGLDGLFGVPSFVSKEHKIYTMIRNLVNVNQESDSDGTSVSEN 125

RESULT 10

Q7YR28 PRELIMINARY; PRT; 491 AA.

AC Q7YR28; (TrEMBLrel. 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Double minute 2 protein MDM2.

GN Name=mdm2;

OS Felis silvestris catus (Cat).

OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.

OX NCBI\_TaxID=9685;

RN [1]

RP SEQUENCE FROM N.A.

RA Miki R., Okuda M., Ma Z., Inokuma H., Onishi T.;

RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB09709; BAC78209.1; -

DR GO; GO:0005730; C:nucleolus; ISS.

DR GO; GO:0005654; C:nucleoplasm; ISS.

DR GO; GO:0017163; F:negative regulator of basal transcription a. . .; ISS.

DR GO; GO:0005515; F:protein binding; ISS.

DR GO; GO:0001222; P:negative regulation of transcription from P. . .; ISS.

DR InterPro; IPR003121; SWIB MDM2.

DR InterPro; IPR001876; Znf\_RanGDP.

DR InterPro; IPR001841; Znf\_Ring.

DR Pfam; PF02201; SWIB; 1.

DR SMART; SM00184; RING; 1.

DR PROSITE; PS01358; ZF\_RANBP2\_1; 1.

DR PROSITE; PS00199; ZF\_RANBP2\_2; 1.

DR PROSITE; PS00089; ZF\_RING\_2; 1.

SQ SEQUENCE 491 AA; 55433 MW; D93E25D638E88934 CRC64;

Query Match 97.3%; Score 538; DB 2; Length 491;

Best Local Similarity 96.3%; Pred. No. 1.7e-49;

Matches 105; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SQPASEQETLVRPKLLKLLKSVGAQKDTYTMKEVFLVGLGYIMTKRLYDEKQHHIVY 60

DB 17 SQPASEQETLVRPKLLKLLKSVGAQKDTYTMKEVFLVGLGYIMTKRLYDEKQHHIVY 76

QY 61 CSNDLLGLDGLFGVPSFVSKEHKIYTMIRNLVNVNQESDSDGTSVSEN 109

DB 77 CSNDLLGLDGLFGVPSFVSKEHKIYTMIRNLVNVNQESDSDGTSVSEN 125

RESULT 11

Q8WYJ2 PRELIMINARY; PRT; 436 AA.

AC Q8WYJ2; (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE MDM2 protein.

GN Name=MDM2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Tamborini E., Della Torre G., Lavarino C., Azzarelli A.,

RA Carpinelli P., Pierotti M.A., Pilotti S.;

RT "Analysis of the molecular species generated by MDM2 gene

RT amplification in liposarcomas.";

RL Int. J. Cancer 92:790-796(2001).

DR EMBL; AF092844; AAL40179.1; -

DR HSP; Q9UMT8; 1YCR.

DR GO; GO:0005730; C:nucleolus; ISS.

DR GO; GO:0005654; C:nucleoplasm; ISS.

DR GO; GO:0017163; F:negative regulator of basal transcription a. . .; ISS.

DR GO; GO:0005515; F:protein binding; ISS.

DR GO; GO:0001222; P:negative regulation of transcription from P. . .; ISS.

DR InterPro; IPR010984; MDM2.

DR InterPro; IPR003121; SWIB MDM2.

DR InterPro; IPR001876; Znf\_RanGDP.

DR InterPro; IPR001841; Znf\_Ring.

DR Pfam; PF02201; SWIB; 1.

DR Pfam; PF00641; zf-RanBP; 1.

DR SMART; SM00184; RING; 1.



DR PROSITE; PS01358; ZF\_RANBP2\_1; 1.  
 DR PROSITE; PS50199; ZF\_RANBP2\_2; 1.  
 DR PROSITE; PS50089; ZF\_RING\_2; 1.  
 SQ SEQUENCE 436 AA; 49248 MW; 3CBF55E98BC4203A CRC64;

Query Match 91.0%; Score 503; DB 2; Length 436;  
 Best Local Similarity 94.3%; Pred. No. 9.1e-46;  
 Matches 99; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKQDTYTKKEVLYFGQYIMTKRLYDEKQOHIVY 60  
 |||  
 Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKQDTYTKKEVLYFGQYIMTKRLYDEKQOHIVY 76  
 |||

Qy 61 CSNDLLGDLFGVPSVKEHKIYIMYIRNLVNVNQESSDSGTS 105  
 |||  
 Db 77 CSNDLLGDLFGVPSVKEHKIYIMYIRNLVNVNQEQENSDELS 121  
 |||

RESULT 12

MDM2\_MOUSE

ID MDM2\_MOUSE STANDARD; PRT; 489 AA.  
 AC P23804; Q61040; Q64330;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein  
 Dm2) (Oncoprotein Mdm2) (Double minute 2 protein).  
 GN Name=Mdm2;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM MDM2-P90).  
 RX MEDLINE=91224107; PubMed=2026149;  
 RA Fakharzadeh S.S., Trusko S.P., George D.L.;  
 RT "Tumorigenic potential associated with enhanced expression of a gene  
 that is amplified in a mouse tumor cell line.";  
 RL EMBO J. 10:1565-1569(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM MDM2-P90).  
 RX STRAIN=129/SV;  
 RA Jones S.N., Ansari-Lari M.A., Hancock A.R., Jones W.J., Gibbs R.A.,  
 RA Donehower L.A., Bradley A.;  
 RT "Genomic organization of the mouse double minute 2 gene.";  
 RL Gene 175:209-213(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM MDM2-P90).  
 RX STRAIN=129/SV;  
 RA MEDLINE=96299630; PubMed=8660994;  
 RA de Oca Luna R.M., Tabor A.D., Eberspaecher H., Hulboy D.L.,  
 RA Worth L.L., Colman M.S., Finlay C.A., Lozano G.;  
 RT "The organization and expression of the mdm2 gene.";  
 RL Genomics 33:352-357(1996).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORMS MDM2-P90 AND MDM2-P76).  
 RX MEDLINE=99175199; PubMed=10075719;  
 RA Saucedo L.J., Myers C.D., Perry M.E.;  
 RT "Multiple murine double minute gene 2 (MDM2) proteins are induced by  
 RT ultraviolet light.";  
 RL J. Biol. Chem. 274:8161-8168(1999).  
 RN [5]  
 RP NUCLEOLAR LOCALIZATION SIGNAL.  
 RX MEDLINE=20180080; PubMed=10713175;  
 RA Weber J.D., Kuo M.-L., Bothner B., DiGiannarino E.L., Kriwacki R.W.,  
 RA Roussel M.F., Sherr C.J.;  
 RT "Cooperative signals governing ARF-mdm2 interaction and nucleolar  
 RT localization of the complex.";  
 RL Mol. Cell. Biol. 20:2517-2528(2000).  
 RN [6]  
 RP PHOSPHORYLATION BY ATM.  
 RX MEDLINE=20079591; PubMed=10611322;

RA Khosravi R., Maya R., Gottlieb T., Oren M., Shiloh Y., Shkedy D.;  
 RT "Rapid ATM-dependent phosphorylation of MDM2 precedes p53 accumulation  
 in response to DNA damage.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 96:14973-14977(1999).  
 CC -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and  
 CC apoptosis by binding its transcriptional activation domain.  
 CC Functions as a ubiquitin ligase E3, in the presence of E1 and E2,  
 CC toward p53 and itself. Permits the nuclear export of p53 and  
 CC targets it for proteasome-mediated proteolysis.  
 CC -!- COTACTOR: Zinc is required for ubiquitin ligase E3 activity.  
 CC -!- SUBUNIT: Binds p53, p73, ARF(p14), ribosomal protein L5 and  
 CC specifically to RNA. Can interact also with retinoblastoma protein  
 CC (RB), E1A-associated protein EP300 and the E2F1 transcription  
 CC factor.  
 CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed  
 CC predominantly in the nucleoplasm. Interacts with ARF(p14)  
 CC results in the localization of both proteins to the nucleolus. The  
 CC nucleolar localization signals in both ARF(p14) and MDM2 may be  
 CC necessary to allow efficient nucleolar localization of both  
 CC proteins.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=Mdm2-p90;  
 CC IsoId=P23804-1; Sequence=Displayed;  
 CC Note=Isoform Mdm2-p76 can also be produced by alternative  
 CC initiation at Met-50 of isoform Mdm2-p90, but is produced more  
 CC efficiently by alternative splicing;  
 CC Name=Mdm2-p76;  
 CC IsoId=P23804-2; Sequence=VSP\_003215;  
 CC Note=Does not bind to p53;  
 CC Event=Alternative initiation;  
 CC Comment=2 isoforms, Mdm2-p90 (shown here) and Mdm2-p76, are  
 CC produced by alternative initiation at Met-1 and Met-50. Isoform  
 CC Mdm2-p76 is produced more efficiently by alternative splicing;  
 CC -!- TISSUE SPECIFICITY: Ubiquitously expressed at low-level throughout  
 CC embryo development and in adult tissues. MDM2-p90 is much more  
 CC abundant than MDM2-p76 in testis, brain, heart, and kidney, but in  
 CC the thymus, spleen, and intestine, the levels of the MDM2 proteins  
 CC are roughly equivalent.  
 CC -!- INDUCTION: By UV light.  
 CC -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its  
 CC G1 arrest and apoptosis functions. It also binds p73 and E2F1.  
 CC Region II contains most of a central acidic region required for  
 CC interaction with ribosomal protein L5 and a putative C4-type zinc  
 CC finger. The RING finger domain which coordinates two molecules of  
 CC zinc interacts specifically with RNA whether or not zinc is  
 CC present and mediates the hetero-oligomerization with MDM4. It is  
 CC also essential for its ubiquitin ligase E3 activity toward p53 and  
 CC itself.  
 CC -!- PTM: Phosphorylated in response to ionizing radiation in an ATM-  
 CC dependent manner.  
 CC -!- DISEASE: The gene for this protein is amplified in a mouse tumor  
 CC cell line.  
 CC -!- SIMILARITY: Belongs to the MDM2 / MDM4 family.  
 CC -!- SIMILARITY: Contains 1 RANBP2-type zinc finger.  
 CC -!- SIMILARITY: Contains 1 RING-type zinc finger.  
 CC -!- SIMILARITY: Contains 1 SWIB domain.  
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 CC -----  
 CC EMBL; X58876; CAA41684.1; -;  
 CC EMBL; U40145; AAA91167.1; -;  
 CC EMBL; U47944; AAB09030.1; -;  
 CC EMBL; U47935; AAB09030.1; JOINED.  
 CC EMBL; U47936; AAB09030.1; JOINED.  
 CC EMBL; U47937; AAB09030.1; JOINED.  
 CC EMBL; U47938; AAB09030.1; JOINED.

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DR EMBL; U47939; AAB09030.1; JOINED.
DR EMBL; U47940; AAB09030.1; JOINED.
DR EMBL; U47941; AAB09030.1; JOINED.
DR EMBL; U47942; AAB09030.1; JOINED.
DR EMBL; U47943; AAB09030.1; JOINED.
DR EMBL; U47934; AAB09031.1; -.
DR PIR; S15349; S15349.
DR HSP; Q9UMT8; 1YCR.
DR MGD; MGI:96952; Mdm2.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IDA.
DR GO; GO:0030163; P:protein catabolism; IDA.
DR GO; GO:0016587; P:protein ubiquitination; IDA.
DR GO; GO:0007089; P:traversing start control point of mitotic c. . .; IDA.
DR InterPro; IPR010984; MDM2.
DR InterPro; IPR003121; SWIB.
DR InterPro; IPR01876; Znf RangDP.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF02201; SWIB; 1.
DR Pfam; PF00641; ZF-RanBP; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01358; ZF_RANBP2_1; 1.
DR PROSITE; PS01199; ZF_RANBP2_2; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS00089; ZF_RING_2; 1.
KW Alternative initiation; Alternative splicing; Ligase; Metal-binding;
KW Nuclear protein; Phosphorylation; Proto-oncogene;
KW Ub1 conjugation pathway; Zinc; Zinc-finger.
FT CHAIN 1 489
FT CHAIN 50 489
FT INIT_MBT 50
FT DOMAIN 27 107
FT DOMAIN 176 182
FT DOMAIN 183 195
FT DOMAIN 203 213
FT DOMAIN 208 302
FT DOMAIN 240 329
FT DOMAIN 221 299
FT ZN_FING 297 326
FT ZN_FING 436 477
FT DOMAIN 464 471
FT VARSPLIC 1 49
FT CONFLICT 203 203
FT CONFLICT 419 419
FT CONFLICT 486 486
FT SEQUENCE 489 AA; 54543 MW; 4ABF49BE92038DF4 CRC64;
Query Match 89.2%; Score 493.5; DB 1; Length 489;
Best Local Similarity 88.1%; Pred. No. 1.1e-44;
Matches 96; Conservative 7; Mismatches 3; Indels 3; Gaps 1;
QY 1 SQIPASEQETLRPKLLILKLLKSGAOKQVYTMKEVLVFLGQYIMTKRLYDEKQOHIVY 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 17 SQIPASEQETLRPKLRPLKLLKLLKSGAQNDDYTMKEVIFIGYIMTKRLYDEKQOHIVY 76
QY 61 CNSDILLGDLFGVPSPFSVKEHRIYTYMYRNVLNVNQQSSDSGTSVSEN 109
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 77 CNSDILLGDLFGVPSPFSVKEHRIYTYMYRNVLNVNQQSSDSGTSVSEN 122
RESULT 13
Q91XK7
ID Q91XK7 PRELIMINARY; PRT; 489 AA.
AC Q91XK7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Mus musculus adult male lung cdna, RIKEN full-length enriched library,

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DE DE clone:1200011P22 product:transformed mouse 3T3 cell double minute 2,
DE full insert sequence (Transformed mouse 3T3 cell double minute 2) (Mus
DE musculus 2 days neonate thymus thymic cells cdna, RIKEN full-length
DE enriched library, clone:E430022B10 product:transformed mouse 3T3 cell
DE double minute 2, full insert sequence).
GN Name=Mdm2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cdna cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cdna collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;
RA The FANTOM Consortium.
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cdna libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuura T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Mouse;

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RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Mouse;  
 RA Strausberg R.;  
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
 RN [9]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NOD; TISSUE=Thymus;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 RA Hori F., Imai K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Katoh H., Kawaji K., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nihi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toya T., Yasunishi G., Muramatsu M., Hayashizaki Y.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK004719; BAB23502.1; -;  
 DR EMBL; BC050902; AAH50902.1; -;  
 DR EMBL; AK088636; BAC40470.1; -;  
 DR HSSP; Q9UNT8; 1YCR.  
 DR MGD; MGI:96952; Mdm2.  
 DR GO; GO:0005730; C:nucleolus; IDA.  
 DR GO; GO:0005515; F:protein binding; IPT.  
 DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IDA.  
 DR GO; GO:0030163; P:protein catabolism; IDA.  
 DR GO; GO:0016567; P:protein ubiquitination; IDA.  
 DR GO; GO:0007089; P:traversing start control point of mitotic c. . .; IDA.  
 DR InterPro; IPR010984; MDM2.  
 DR InterPro; IPR003121; SWIB\_MDM2.  
 DR InterPro; IPR001876; Znf\_RanGDP.  
 DR InterPro; IPR001841; Znf\_ring.  
 DR Pfam; PF02201; SWIB; 1.  
 DR Pfam; PF06641; zf-RanBP; 1.  
 DR SMART; SM00184; RING; 1.  
 DR PROSITE; PS01358; ZF\_RANBP2\_1; 1.  
 DR PROSITE; PS50199; ZF\_RANBP2\_2; 1.  
 DR PROSITE; PS50089; ZF\_RING\_2; 1.  
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 Query Match 89.2%; Score 493.5; DB 2; Length 489;  
 Best Local Similarity 88.1%; Pred. No. 1.1e-44;  
 Matches 96; Conservative 7; Mismatches 3; Indels 3; Gaps 1;  
 Qy 1 SQIPASEQETLVPRPKLLKLLKSVGAKQDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 60  
 Db 17 SQIPASEQETLVPRPKLLKLLKSVGAKQDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76  
 Qy 61 CSNDLLGDLFGVPSFVSKHRKIYTMIRNLV 109

Db 77 CSNDLLGDLFGVPSFVSKHRKIYTMIRNLVAVSQ---DSGTSLS 122  
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 Q8WYJ3 PRELIMINARY; PRT; 118 AA.  
 ID Q8WYJ3  
 AC Q8WYJ3  
 DT 01-MAR-2002 (TRENBLrel. 20, Created)  
 DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
 DE MDM2 protein (Fragment).  
 GN Name=MDM2;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21248713; PubMed=11351297;  
 RA Tamborini E., Della Torre G., Lavarino C., Azzarelli A.,  
 RA Carpinelli P., Pierotti M.A., Pilotti S.;  
 RT "Analysis of the molecular species generated by MDM2 gene  
 RT amplification in liposarcomas";  
 RL Int. J. Cancer 92:790-796(2001).  
 DR EMBL; AF092843; AAL40178.1; -;  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR InterPro; IPR010984; MDM2.  
 DR InterPro; IPR003121; SWIB\_MDM2.  
 DR Pfam; PF02201; SWIB; 1.  
 DR NON\_TER 118 118  
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 Qy 61 CSNDLLGDLFGVPSFVSKHRKIYTMIRNLV 93  
 Db 77 CSNDLLGDLFGVPSFVSKHRKIYTMIRNLV 109  
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 MDM2\_MESAU  
 ID MDM2\_MESAU STANDARD; PRT; 466 AA.  
 AC Q60524;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein  
 DE Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Fragment).  
 GN Name=MDM2;  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus.  
 OX NCBI\_TaxID=10036;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=Pancras;  
 RA MEDLINE=95300112; PubMed=7780969;  
 RA Chang K.W., Laconi S., Mangold K.A., Hubchak S., Scarpelli D.G.;  
 RT "Multiple genetic alterations in hamster pancreatic ductal  
 RT adenocarcinomas.";  
 RL Cancer Res. 55:2560-2568(1995).  
 CC -1- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and  
 CC apoptosis by binding its transcriptional activation domain.  
 CC Functions as a ubiquitin ligase E3, in the presence of E1 and E2,  
 CC toward p53 and itself. Permits the nuclear export of p53 and

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68 CSNDLGLDIFGVPSFKDHRKIHIMIYRNLVVVSQOETLQSGTSVSES 116

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targets it for proteasome-mediated proteolysis (By similarity).  
-|- COPACITOR: Zinc is required for ubiquitin ligase E3 activity (By similarity).  
-|- SUBUNIT: Binds p53, p73, ARF (p14), ribosomal protein L5 and specifically to RNA. Can interact also with retinoblastoma protein (RB), E1A-associated protein EP300 and the E2F1 transcription factor (By similarity).  
-|- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed predominantly in the nucleoplasm (By similarity).  
-|- DOMAIN: Region I is sufficient for binding p53 and inhibiting its G1 arrest and apoptosis functions. It also binds p73 and E2F1. Region II contains most of a central acidic region required for interaction with ribosomal protein L5 and a putative C4-type zinc finger. The RING finger domain which coordinates two molecules of zinc interacts specifically with RNA whether or not zinc is present and mediates the hetero-oligomerization with MDM4. It is also essential for its ubiquitin ligase E3 activity toward p53 and itself (By similarity).  
-|- DISEASE: The gene for this protein is overexpressed in some tumors.  
-|- SIMILARITY: Belongs to the MDM2 / MDM4 family.  
-|- SIMILARITY: Contains 1 RanBP2-type zinc finger.  
-|- SIMILARITY: Contains 1 RING-type zinc finger.  
-|- SIMILARITY: Contains 1 SWIB domain.

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--CC					EMBL; UI0982; AAC52425.1;	- -	
DR	HSPB	Q9UMT8,	LYCR.				
DR	InterPro:	IPR010984;	MDM2.				
DR	InterPro:	IPR003121;	SWIB.				
DR	InterPro:	IPR001876;	Znf_RanGDP.				
DR	InterPro:	IPR001841;	Znf_ring.				
DR	Pfam:	PF02201;	SWIB; l_				
DR	Pfam:	PF00641;	zf-RanBP; l.				
DR	SMART,	SM00184;	RING; l.				
DR	PROSITE;	PS01358;	ZF_RANBP2_1; l.				
DR	PROSITE;	PS50199;	ZF_RANBP2_2; l.				
DR	PROSITE;	PS00518;	ZF_RING_1; FALSE_NEG.				
DR	PROSITE;	PS50089;	ZF_RING_2; l.				
DR	KW	Ligase;	Metal-binding; Nuclear protein; Proto-oncogene;				
XW	Ubl conjugation pathway;	Zinc; Zinc-finger.					
FT	NON_TER	l					
FT	DOMAIN	19	98	SMB.	Nuclear localization signal (Potential).		
FT	DOMAIN	169	175	Nuclear export signal.			
FT	DOMAIN	176	188				
FT	DOMAIN	196	201	Poly-Ser.			
FT	DOMAIN	196	290	ARP-binding.			
FT	DOMAIN	228	317	Region II.			
FT	DOMAIN	209	287	Asp/Glu-rich (acidic).			
FT	ZN_FING	285	314	RanBP2-type.			
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Db	9	SQIPASQETLVRPKPLFLKLLKSVGAKQDITYNKEIL-SWQYIMTKRLYDKQQHIVY	67
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OM protein - protein search, using sw model

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Title: US-10-822-254-2  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	553	100.0	188	4	US-09-603-052-4
2	553	100.0	491	1	US-07-903-103-2
3	553	100.0	491	1	US-08-044-619A-2
4	553	100.0	491	1	US-08-283-911-2
5	553	100.0	491	1	US-08-245-500A-3
6	553	100.0	491	1	US-08-390-546-3
7	553	100.0	491	1	US-08-390-479A-3
8	553	100.0	491	1	US-08-557-393-3
9	553	100.0	491	1	US-08-390-516C-3
10	553	100.0	491	1	US-08-390-517A-3
11	553	100.0	491	1	US-08-390-515A-3
12	553	100.0	491	2	US-08-801-718-3
13	553	100.0	491	3	US-09-170-159A-3
14	553	100.0	491	4	US-09-480-718-4
15	536.5	97.0	216	3	US-09-510-252-4
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23	493.5	89.2	489	1	US-08-390-516C-5
24	493.5	89.2	489	1	US-08-390-517A-5
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28	493.5	89.2	489	4	US-09-480-718-46	Sequence 46, Appl
29	176	31.8	243	4	US-09-786-702-2	Sequence 2, Appl
30	70.5	12.7	420	4	US-09-270-767-43304	Sequence 43304, A
31	70	12.7	62	4	US-09-248-796A-24446	Sequence 24446, A
32	68.5	12.4	244	4	US-09-543-681A-6675	Sequence 6675, Ap
33	68	12.3	2938	5	PCT-US94-00198-3	Sequence 3, Appl
34	64.5	11.7	107	3	US-09-187-859-35	Sequence 35, Appl
35	64.5	11.7	107	3	US-09-187-859-36	Sequence 36, Appl
36	64.5	11.7	107	4	US-09-839-542B-35	Sequence 35, Appl
37	64.5	11.7	107	4	US-09-839-542B-36	Sequence 36, Appl
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40	64.5	11.7	108	4	US-09-535-852-54	Sequence 54, Appl
41	64.5	11.7	108	4	US-09-535-852-57	Sequence 57, Appl
42	64.5	11.7	271	3	US-09-134-001C-3549	Sequence 3549, Ap
43	64.5	11.7	485	3	US-08-378-313-25	Sequence 25, Appl
44	64.5	11.7	485	3	US-08-378-313-27	Sequence 27, Appl
45	64.5	11.7	485	3	US-08-378-313-32	Sequence 32, Appl

## ALIGNMENTS

### RESULT 1

US-09-603-052-4  
; Sequence 4, Application US/09603052  
; Patent No. 6492116  
; GENERAL INFORMATION:  
; APPLICANT: Chene, Patrick  
; APPLICANT: Hochkeppel, Heinz-Kurt  
; TITLE OF INVENTION: Assay for identifying inhibitors of the interaction  
; FILE REFERENCE: MEMB26.001C1  
; CURRENT APPLICATION NUMBER: US/09/603,052  
; PRIOR FILING DATE: 2000-06-26  
; PRIOR APPLICATION NUMBER: EP 95810576.9  
; PRIOR FILING DATE: 1995-09-18  
; PRIOR APPLICATION NUMBER: PCT/EP96/03957  
; PRIOR FILING DATE: 1996-09-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 188  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-603-052-4

Query Match	100.0%;	Score	553;	DB	4;	Length	188;
Best Local Similarity	100.0%;	Pred. No.	4e-62;	Mismatches	0;	Indels	0;
Matches	109;	Conservative	0;	Indels	0;	Gaps	0;
Oy	1	SOIPASQETLVVRPKPLLLKLSVGAQKDTYTMKEVL	FYLGQYIMTKRLYDEKQOHIVY	60			
Db	17	SOIPASQETLVVRPKPLLLKLSVGAQKDTYTMKEVL	FYLGQYIMTKRLYDEKQOHIVY	76			
Oy	61	CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVNQESSDGSSTSVSEN	109				
Db	77	CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVNQESSDGSSTSVSEN	125				

### RESULT 2

US-07-903-103-2  
; Sequence 2, Application US/07903103  
; Patent No. 5411860  
; GENERAL INFORMATION:  
; APPLICANT: VOGELSTEIN, BERT  
; APPLICANT: KINZLER, KENNETH  
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
; TITLE OF INVENTION: HUMAN TUMORS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
; STREET: 1001 G ST., N.W.

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CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/903,103
FILING DATE: 19920623
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/867,840
FILING DATE: 07-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.40148
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-903-103-2

Query Match 100.0%; Score 553; DB 1; Length 491;
Best Local Similarity 100.0%; Pred.No.1.4e-61; Indels 0; Gaps 0;
Matches 109; Conservative 0; Mismatches 0;

QY 1 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLFVLGQYIMTKELYDEKQOHIVY 60
Db 17 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLFVLGQYIMTKELYDEKQOHIVY 76

QY 61 CSNDLLGDLFGVPFSFVKRHKIYTMIRNLVNVNQESSDSGTSVSEN 109
Db 77 CSNDLLGDLFGVPFSFVKRHKIYTMIRNLVNVNQESSDSGTSVSEN 125

RESULT 3
US-08-044-619A-2
Sequence 2, Application US/08044619A
Patent No. 5420263
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY
APPLICANT: 720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
TITLE OF INVENTION: HUMAN TUMORS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
STREET: 1001 G ST., N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/044,619A
FILING DATE: 07-APR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/903,103

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; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-283-911-2

Query Match 100.0%; Score 553; DB 1; Length 491;
Best Local Similarity 100.0%; Pred. No. 1.4e-61;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 60
Db 17 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPFSVKEHRKIYTMIRNVLVVNQESSDGSVSEN 109
Db 77 CSNDLLGDLFGVPFSVKEHRKIYTMIRNVLVVNQESSDGSVSEN 125

RESULT 5
US-08-245-500A-3
; Sequence 3, Application US/08245500A
; Patent No. 5550023
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/245,500A
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BMB UT
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-245-500A-3

Query Match 100.0%; Score 553; DB 1; Length 491;
Best Local Similarity 100.0%; Pred. No. 1.4e-61;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 60
Db 17 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPFSVKEHRKIYTMIRNVLVVNQESSDGSVSEN 109
Db 77 CSNDLLGDLFGVPFSVKEHRKIYTMIRNVLVVNQESSDGSVSEN 125
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Db 77 CSNDLLGDLFGVPFSVKEHRKIYTMIRNVLVVNQESSDGSVSEN 125

RESULT 6
US-08-390-546-3
; Sequence 3, Application US/08390546
; Patent No. 5606044
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,546
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BMB UT
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-390-546-3

Query Match 100.0%; Score 553; DB 1; Length 491;
Best Local Similarity 100.0%; Pred. No. 1.4e-61;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 60
Db 17 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPFSVKEHRKIYTMIRNVLVVNQESSDGSVSEN 109
Db 77 CSNDLLGDLFGVPFSVKEHRKIYTMIRNVLVVNQESSDGSVSEN 125

RESULT 7
US-08-390-479A-3
; Sequence 3, Application US/08390479A
; Patent No. 5618921
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
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; ADDRESSEE: BANNER & WITCOFF, LTD.
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,479A
; FILING DATE: 02-FEB-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.48992
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BMB UT
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-390-479A-3
;
; Query Match 100.0%; Score 553; DB 1; Length 491;
; Best Local Similarity 100.0%; Pred. No. 1.4e-61;
; Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 SQIPASEQETLVVRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQHHIVY 60
; DB 17 SQIPASEQETLVVRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQHHIVY 76
;
; QY 61 CSNDLLGDLFGVPFSFVKHRIYTYMYRNLVVNQESSDSGTSVSEN 109
; DB 77 CSNDLLGDLFGVPFSFVKHRIYTYMYRNLVVNQESSDSGTSVSEN 125
;
; RESULT 8
; US-08-557-393-3
; Sequence 3, Application US/08557393
; Patent No. 5702903
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,393
; FILING DATE: 13-NOV-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;
; ADDRESSSEE: BANNER & WITCOFF, LTD.
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,479A
; FILING DATE: 02-FEB-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.48992
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BMB UT
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-390-479A-3
;
; Query Match 100.0%; Score 553; DB 1; Length 491;
; Best Local Similarity 100.0%; Pred. No. 1.4e-61;
; Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 1 SQIPASEQETLVVRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQHHIVY 60
; DB 17 SQIPASEQETLVVRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQHHIVY 76
;
; QY 61 CSNDLLGDLFGVPFSFVKHRIYTYMYRNLVVNQESSDSGTSVSEN 109
; DB 77 CSNDLLGDLFGVPFSFVKHRIYTYMYRNLVVNQESSDSGTSVSEN 125
;
; RESULT 9
; US-08-390-516C-3
; Sequence 3, Application US/08390516C
; Patent No. 5708136
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,516C
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BMB UT
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-557-393-3
;
; Query Match 100.0%; Score 553; DB 1; Length 491;
; Best Local Similarity 100.0%; Pred. No. 1.4e-61;
; Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
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; DB 17 SQIPASEQETLVVRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQHHIVY 76
;
; QY 61 CSNDLLGDLFGVPFSFVKHRIYTYMYRNLVVNQESSDSGTSVSEN 109
; DB 77 CSNDLLGDLFGVPFSFVKHRIYTYMYRNLVVNQESSDSGTSVSEN 125
;
; RESULT 9
; US-08-390-516C-3
; Sequence 3, Application US/08390516C
; Patent No. 5708136
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,516C
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BMB UT
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-557-393-3
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## RESULT 11

;; COUNTRY: USA  
;; ZIP: 20001  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/801,718  
;; FILING DATE: 14-FEB-1997  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/390,515  
;; FILING DATE: 07-APR-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: KAGAN, SARAH A.  
;; REGISTRATION NUMBER: 32,141  
;; REFERENCE/DOCKET NUMBER: 01107.42798  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-508-9100  
;; TELEFAX: 202-508-9299  
;; TELEX: 197430 BMB UT  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 491 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-801-718-3

Query Match 100.0%; Score 553; DB 2; Length 491;  
Best Local Similarity 100.0%; Pred. No. 1.4e-61;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQHHIVY 60  
Db 17 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQHHIVY 76

Qy 61 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVVNQQSSDSGTSVSEN 109  
Db 77 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVVNQQSSDSGTSVSEN 125

RESULT 13  
US-09-170-159A-3  
; Sequence 3, Application US/09170159A  
; Patent No. 6399755  
; GENERAL INFORMATION:  
; APPLICANT: BURRELL, MARILEE  
; HILL, DAVID E.  
; KINZLER, KENNETH W.  
; VOGELSTEIN, BERT  
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
; HUMAN TUMORS  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
; STREET: 1001 G STREET, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/170,159A  
; FILING DATE: 13-Oct-1998  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KAGAN, SARAH A.

;; REGISTRATION NUMBER: 32,141  
;; REFERENCE/DOCKET NUMBER: 01107.42798  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-508-9100  
;; TELEFAX: 202-508-9299  
;; TELEX: 197430 BMB UT  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 491 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-170-159A-3

Query Match 100.0%; Score 553; DB 3; Length 491;  
Best Local Similarity 100.0%; Pred. No. 1.4e-61;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQHHIVY 60  
Db 17 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQHHIVY 76

Qy 61 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVVNQQSSDSGTSVSEN 109  
Db 77 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVVNQQSSDSGTSVSEN 125

RESULT 14  
US-09-480-718-44  
; Sequence 44, Application US/09480718  
; Patent No. 6407062  
; GENERAL INFORMATION:  
; APPLICANT: Sherr, Charles J  
; APPLICANT: Quelle, Dawn E  
; APPLICANT: Weber, Jason D  
; APPLICANT: Rousset, Martine F  
; APPLICANT: Frederique, Zindy  
; TITLE OF INVENTION: ARF-19, A NOVEL REGULATOR OF THE MAMMALIAN CELL CYCLE  
; FILE REFERENCE: 1340-1-023 CIP 1  
; CURRENT APPLICATION NUMBER: US/09/480,718  
; CURRENT FILING DATE: 2000-01-07  
; EARLIER APPLICATION NUMBER: 09/129,855  
; EARLIER FILING DATE: 1998-08-06  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 44  
; LENGTH: 491  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-480-718-44

Query Match 100.0%; Score 553; DB 4; Length 491;  
Best Local Similarity 100.0%; Pred. No. 1.4e-61;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQHHIVY 60  
Db 17 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQHHIVY 76

Qy 61 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVVNQQSSDSGTSVSEN 109  
Db 77 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVVNQQSSDSGTSVSEN 125

RESULT 15  
US-09-510-252-4  
; Sequence 4, Application US/09510252  
; Patent No. 6372490  
; GENERAL INFORMATION:  
; APPLICANT: Nandabalan, Krishnan  
; APPLICANT: Yang, Meijia  
; APPLICANT: Schulz, Vincent

```

; APPLICANT: CuraGen Corporation
; TITLE OF INVENTION: MDM INTERACTING PROTEIN AND METHODS OF USE THEREOF
; FILE REFERENCE: 15966-524 MDM US
; CURRENT APPLICATION NUMBER: US/09/510,252
; CURRENT FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: USSN 60/121,192
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: USSN 60/122,643
; PRIOR FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-510-252-4

Query Match      97.0%; Score 536.5; DB 3; Length 216;
Best Local Similarity 99.1%; Pred. No. 5.9e-60;
Matches 108; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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      Db      17  SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 75

Qy      61  CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVNQESSDSGTSVSEN 109
      Db      76  CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVNQESSDSGTSVSEN 124

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Job time : 24.2 secs

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OM protein - protein search, using sw model

Run on: January 27, 2005, 17:59:36 ; Search time 69.4 Seconds  
(without alignments)  
567.443 Million cell updates/sec

Title: US-10-822-254-2

Perfect score: 553  
Sequence: 1 SQIPASQETLVRPKPLLLK.....NLVVNQESSDSGTSVSEN 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
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- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
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- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
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- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
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- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	553	100.0	491	9	US-09-888-077-1
2	553	100.0	491	9	US-09-956-425-8
3	553	100.0	491	10	US-09-029-327-2
4	553	100.0	491	11	US-09-966-724-2
5	553	100.0	491	15	US-10-422-536-137
6	553	100.0	491	15	US-10-232-951-35
7	553	100.0	491	17	US-10-685-838-1
8	553	100.0	491	17	US-10-724-225-2
9	553	100.0	491	17	US-10-489-802-8
10	553	100.0	491	17	US-10-723-860-2236
11	536.5	97.0	216	13	US-10-057-510-4
12	527.5	95.4	522	15	US-10-287-222-15
13	527.5	95.4	522	15	US-10-287-226-380

14	493.5	89.2	489	9	US-09-956-425-6	Sequence 6, Appli
15	493.5	89.2	489	11	US-09-966-724-4	Sequence 4, Appli
16	493.5	89.2	489	17	US-10-489-802-6	Sequence 6, Appli
17	486	87.9	95	17	US-10-685-838-2	Sequence 2, Appli
18	477	86.3	95	17	US-10-685-838-4	Sequence 4, Appli
19	473	85.5	92	17	US-10-685-838-3	Sequence 3, Appli
20	314	56.8	59	14	US-10-211-088-143	Sequence 143, App
21	76	13.7	472	14	US-10-369-493-16585	Sequence 16585, A
22	76	13.7	473	15	US-10-282-122A-45311	Sequence 45311, A
23	76	13.7	967	15	US-10-282-122A-59020	Sequence 59020, A
24	72.5	13.1	578	16	US-10-437-963-174237	Sequence 174237, A
25	72	13.0	969	15	US-10-335-977-7409	Sequence 7409, Ap
26	72	13.0	972	15	US-10-335-977-7410	Sequence 7410, Ap
27	70.5	12.7	225	15	US-10-282-122A-52429	Sequence 52429, A
28	70.5	12.7	328	17	US-10-425-115-191466	Sequence 191466, A
29	70.5	12.7	422	14	US-10-369-493-7027	Sequence 7027, Ap
30	70	12.7	613	16	US-10-437-963-113326	Sequence 113326, A
31	69.5	12.6	277	15	US-10-282-122A-75363	Sequence 75363, A
32	68.5	12.4	291	15	US-10-425-114-59872	Sequence 59872, A
33	68.5	12.4	291	17	US-10-425-115-191465	Sequence 191465, A
34	68.5	12.4	709	15	US-10-282-122A-63455	Sequence 63455, A
35	68	12.3	3092	9	US-09-801-368-172	Sequence 172, App
36	68	12.3	3092	14	US-10-369-493-1470	Sequence 1470, Ap
37	67.5	12.2	438	10	US-09-769-787-48	Sequence 48, Appli
38	67.5	12.2	467	14	US-10-362-774-3	Sequence 3, Appli
39	67.5	12.2	467	14	US-10-369-493-6071	Sequence 6071, Ap
40	67	12.1	404	15	US-10-282-122A-61064	Sequence 61064, A
41	67	12.1	701	15	US-10-282-122A-53065	Sequence 53065, A
42	67	12.1	1031	16	US-10-437-963-189155	Sequence 189155, A
43	66.5	12.0	498	14	US-10-369-493-20438	Sequence 20438, A
44	66.5	12.0	839	14	US-10-295-027-326	Sequence 326, App
45	66.5	12.0	896	14	US-10-176-847-98	Sequence 98, Appli

#### ALIGNMENTS

RESULT 1  
US-09-888-077-1  
; Sequence 1, Application US/09888077  
; Patent No. US2002003181A1  
; GENERAL INFORMATION:  
; APPLICANT: Konal, Ze'ev  
; APPLICANT: Fuchs, Serge  
; TITLE OF INVENTION: Modification of Mdm2 Activity  
; FILE REFERENCE: 2420/1H195-US1  
; CURRENT APPLICATION NUMBER: US/09/888,077  
; PRIOR FILING DATE: 2001-06-22  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 491  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-888-077-1

Query Match	100.0%;	Score	553;	DB	9;	Length	491;
Best Local Similarity	100.0%;	Pred. No.	1.3e-57;				
Matches	109;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Oy	1	SOIPASQETLVRPKPLLLKLSVGAQKQTYTMTKVELFYLGVQYIMTKRLYDEKQOHIVY	60				
Db	17	SOIPASQETLVRPKPLLLKLSVGAQKQTYTMTKVELFYLGVQYIMTKRLYDEKQOHIVY	76				
Oy	61	CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVNQESSDSGTSVSEN	109				
Db	77	CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVNQESSDSGTSVSEN	125				

RESULT 2  
US-09-956-425-8

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; Sequence 8, Application US/09956425
; Patent No. US20020045192A1
; GENERAL INFORMATION:
; APPLICANT: Kriwacki, Richard
; APPLICANT: Bothner, Brian
; APPLICANT: Lewis, William
; TITLE OF INVENTION: Araf and Hdm2 Interaction Domains and Method of Use Thereof
; FILE REFERENCE: 1340/1/035
; CURRENT APPLICATION NUMBER: US/09/956,425
; CURRENT FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 8
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-956-425-8

Query Match      100.0%; Score 553; DB 9; Length 491;
Best Local Similarity 100.0%; Pred. No. 1.3e-57;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 60
Db 17 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPSFVKHEHKIYTMIRNLVVVNNQOESSDSGTSVSEN 109
Db 77 CSNDLLGDLFGVPSFVKHEHKIYTMIRNLVVVNNQOESSDSGTSVSEN 125

RESULT 3
US-09-029-327-2
; Sequence 2, Application US/09029327
; Publication No. US20030060432A1
; GENERAL INFORMATION:
; APPLICANT: TOCQUE, Bruno
; APPLICANT: WASYLK, Bohdan
; APPLICANT: DUBS-POTERSZMAN,
; APPLICANT: Marie-Christine
; TITLE OF INVENTION: ANTAGONISTS OF THE ONCOGENIC ACTIVITY OF
; TITLE OF INVENTION: THE PROTEIN MDM2, AND USE THEREOF IN THE TREATMENT OF
; TITLE OF INVENTION: CANCERS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, Mailstop 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/029,327
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 96/01340
; FILING DATE: 02-SEP-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO FR95/10331
; FILING DATE: 04-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fehlner Esq., Paul F.
; REGISTRATION NUMBER: 35,135
; REFERENCE/DOCKET NUMBER: ST95050-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-029-327-2

Query Match      100.0%; Score 553; DB 10; Length 491;
Best Local Similarity 100.0%; Pred. No. 1.3e-57;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 60
Db 17 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPSFVKHEHKIYTMIRNLVVVNNQOESSDSGTSVSEN 109
Db 77 CSNDLLGDLFGVPSFVKHEHKIYTMIRNLVVVNNQOESSDSGTSVSEN 125

RESULT 4
US-09-966-724-2
; Sequence 2, Application US/09966724
; Publication No. US20040170971A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G ST., N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4537
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/966,724
; FILING DATE: 01-Oct-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/044,619
; FILING DATE: 2001-10-01
; APPLICATION NUMBER: US 07/867,840
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.40148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-966-724-2

Query Match      100.0%; Score 553; DB 11; Length 491;
Best Local Similarity 100.0%; Pred. No. 1.3e-57;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	1	SOIPASEQETLVNRPKPLLKLLKLLKLVCAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY	60
Db	17	SOIPASEQETLVNRPKPLLKLLKLVCAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY	76
Qy	61	CSNDLLGDLFGVPSPFVKVHKRIYTIMYRNLVVVAQQSSDSGTSVSEN	109
Db	77	CSNDLLGDLFGVPSPFVKVHKRIYTIMYRNLVVVAQQSSDSGTSVSEN	125

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RESULT 5
US-10-422-536-137
; Sequence 137, Application US/10422536
; Publication No. US20040014100A1
; GENERAL INFORMATION:
; APPLICANT: Kinsella, Todd
; APPLICANT: Lorens, James
; APPLICANT: Pray, Todd
; APPLICANT: Bennett, Mark
; TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR INHIBITING
; TITLE OF INVENTION: PROTEIN-PROTEIN INTERACTION
; FILE REFERENCE: A-71433-1/AMP/CYO
; CURRENT APPLICATION NUMBER: US/10/422,536
; CURRENT FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: US 60/187,130
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 09/800,770
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: US 10/232,758
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 137
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-422-536-137

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RESULT 6
US-10-232-951-35
; Sequence 35, Application US/10232951
; Publication No. US20040043386A1
; GENERAL INFORMATION:
; APPLICANT: Pray, Todd
; APPLICANT: Wong, Brian
; APPLICANT: Bennett, Mark
; APPLICANT: Parlati, Francesco
; APPLICANT: Rigel Pharmaceuticals, Incorporated
; TITLE OF INVENTION: Methods and Compositions for Functional Ubiquitin
; TITLE OF INVENTION: Assays
; FILE REFERENCE: 021044-006800US
; CURRENT APPLICATION NUMBER: US/10/232,951
; CURRENT FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: E3 ubiquitin ligating agent mouse double minute 2

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; OTHER INFORMATION: (mdm2) homolog full length protein isoform, mouse
; OTHER INFORMATION: p53-binding protein (MDM2) homolog, transcript
; OTHER INFORMATION: variant MDM2, transformed 3T3 cell double minute 2,
; OTHER INFORMATION: Mdm2 cDNA
US-10-232-951-35

Query Match          100.0%; Score 553; DB 15; Length 491;
Best Local Similarity 100.0%; Pred. No. 1.3e-57;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 60
Db 17 SQIPASEQETLVRPKPLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPFSFSVKEHRKIYTIYRNLVVNVNQESSDSDGTSVSEN 109
Db 77 CSNDLLGDLFGVPFSFSVKEHRKIYTIYRNLVVNVNQESSDSDGTSVSEN 125

RESULT 7
US-10-685-838-1
; Sequence 1, Application US/10685838
; Publication No. US20040197893A1
; GENERAL INFORMATION:
; APPLICANT: SHUBERT, CARSTEN
; APPLICANT: GRASBERGER, BRUCE
; APPLICANT: MAGUIRE, DIANE
; APPLICANT: DECKMAN, INGRID
; APPLICANT: SPURLINO, JOHN
; TITLE OF INVENTION: HDM2-INHIBITOR COMPLEXES AND USES THEREOF
; FILE REFERENCE: PRD-2137-USANP
; CURRENT APPLICATION NUMBER: US/10/685,838
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: 60/418,350
; PRIOR FILING DATE: 2002-10-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-685-838-1

Query Match          100.0%; Score 553; DB 17; Length 491;
Best Local Similarity 100.0%; Pred. No. 1.3e-57;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 60
Db 17 SQIPASEQETLVRPKPLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPFSFSVKEHRKIYTIYRNLVVNVNQESSDSDGTSVSEN 109
Db 77 CSNDLLGDLFGVPFSFSVKEHRKIYTIYRNLVVNVNQESSDSDGTSVSEN 125

RESULT 8
US-10-724-225-2
; Sequence 2, Application US/10724225
; Publication No. US20040209834A1
; GENERAL INFORMATION:
; APPLICANT: TOCOUE, Bruno
; APPLICANT: WASLYLK, Bohdan
; APPLICANT: DUBS-POTERSZMAN,
; Marie-Christine
; TITLE OF INVENTION: ANTAGONISTS OF THE ONCOGENIC ACTIVITY OF
; THE PROTEIN MDM2, AND USE THEREOF IN THE TREATMENT
; OF CANCERS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, Mailstop 3C43
; CITY: Collegeville

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STATE: PA  
COUNTRY: USA  
ZIP: 19426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/724,225  
FILING DATE: 01-Dec-2003  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/029,327  
FILING DATE: <Unknown>  
APPLICATION NUMBER: FR 96/01340  
FILING DATE: 02-SEP-1996  
APPLICATION NUMBER: WO FR95/10331  
FILING DATE: 04-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Fehlnher Esq., Paul F.  
REGISTRATION NUMBER: 35,135  
REFERENCE/DOCKET NUMBER: ST95050-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 454-3839  
TELEFAX: (610) 454-3808  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 491 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-724-225-2

Query Match 100.0%; Score 553; DB 17; Length 491;  
Best Local Similarity 100.0%; Pred. No. 1.3e-57;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 60  
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76  
Qy 61 CSNDLLGDLFGVPFSFVKHRKIYTMIRNLVVVNQESSDSTSVSEN 109  
Db 77 CSNDLLGDLFGVPFSFVKHRKIYTMIRNLVVVNQESSDSTSVSEN 125

RESULT 9  
US-10-489-802-8  
Sequence 8, Application US/10489802  
Publication No. US20040248198A1  
GENERAL INFORMATION:  
APPLICANT: St. Jude Children's Research Hospital, Inc.  
APPLICANT: Kriwacki, Richard  
APPLICANT: Bothner, Brian  
APPLICANT: Lewis, William  
TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and  
FILE REFERENCE: 44158/243642  
CURRENT APPLICATION NUMBER: US/10/489,802  
CURRENT FILING DATE: 2004-03-16  
PRIOR APPLICATION NUMBER: US 09/956,425  
PRIOR FILING DATE: 2001-09-19  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 491  
TYPE: PRP  
ORGANISM: Homo sapiens  
US-10-489-802-8

Query Match 100.0%; Score 553; DB 17; Length 491;

Best Local Similarity 100.0%; Pred. No. 1.3e-57;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 60  
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76  
Qy 61 CSNDLLGDLFGVPFSFVKHRKIYTMIRNLVVVNQESSDSTSVSEN 109  
Db 77 CSNDLLGDLFGVPFSFVKHRKIYTMIRNLVVVNQESSDSTSVSEN 125  
RESULT 10  
US-10-723-860-2236  
Sequence 2236, Application US/10723860  
Publication No. US20040253606A1  
GENERAL INFORMATION:  
APPLICANT: Aziz, Natasha  
APPLICANT: Ginsburg, Wendy M.  
APPLICANT: Zlotnik, Albert  
TITLE OF INVENTION: Methods for Diagnosis of Soft Tissue Sarcoma, Compositions &  
FILE REFERENCE: 05882.0193.NPUS01  
CURRENT APPLICATION NUMBER: US/10/723,860  
CURRENT FILING DATE: 2003-11-26  
PRIOR APPLICATION NUMBER: 60/429,739  
PRIOR FILING DATE: 2002-11-26  
NUMBER OF SEQ ID NOS: 8393  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 2236  
LENGTH: 491  
TYPE: PRP  
ORGANISM: Homo sapiens  
US-10-723-860-2236

Query Match 100.0%; Score 553; DB 17; Length 491;  
Best Local Similarity 100.0%; Pred. No. 1.3e-57;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 60  
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76  
Qy 61 CSNDLLGDLFGVPFSFVKHRKIYTMIRNLVVVNQESSDSTSVSEN 109  
Db 77 CSNDLLGDLFGVPFSFVKHRKIYTMIRNLVVVNQESSDSTSVSEN 125

RESULT 11  
US-10-057-510-4  
Sequence 4, Application US/10057510  
Publication No. US20020098580A1  
GENERAL INFORMATION:  
APPLICANT: Nandabalan, Krishnan  
APPLICANT: Yang, Meijia  
APPLICANT: Schulz, Vincent  
APPLICANT: Curagen Corporation  
TITLE OF INVENTION: MDM INTERACTING PROTEIN AND METHODS OF USE THEREOF  
FILE REFERENCE: 15966-524 MDM US  
CURRENT APPLICATION NUMBER: US/10/057,510  
CURRENT FILING DATE: 2002-01-25  
PRIOR APPLICATION NUMBER: USSN 09/510,252  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: USSN 60/121,192  
PRIOR FILING DATE: 1999-02-23  
PRIOR APPLICATION NUMBER: USSN 60/122,643  
PRIOR FILING DATE: 1999-03-03  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4  
LENGTH: 216  
TYPE: PRP  
ORGANISM: Homo sapiens



## US-10-057-510-4

Query Match 97.0%; Score 536.5; DB 13; Length 216;  
Best Local Similarity 99.1%; Pred. No. 4.4e-56;  
Matches 108; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 SQIPASQETLVRPKPLLLKLLKSVGAQKQDTYTKKVLVYLGQYIMTKRLYDEKQOHHIVY 60  
Dy 17 SQIPASQETLVRPKPLLLKLLKSVGAQKQDTYTKKVLVYLGQYIMTKRLYDEKQOHHIVY 75  
Qy 61 CSNDLLGDLFGVPFSFVKHHRKIYTMIRNLVNVNQESSDSGTSVSEN 109  
Dy 76 CSNDLLGDLFGVPFSFVKHHRKIYTMIRNLVNVNQESSDSGTSVSEN 124

## RESULT 12

US-10-287-226-380  
Sequence 380, Application US/10287226  
Publication No. US20040086875A1

GENERAL INFORMATION:  
APPLICANT: Agee, Michele L.,

APPLICANT: Alsobrook, John P.,  
APPLICANT: Berghs, Constance,  
APPLICANT: Boldog, Ference,  
APPLICANT: Burgess, Catherine E.,  
APPLICANT: Chant, John S.,  
APPLICANT: Chaudhuri, Amitabha,  
APPLICANT: DiPippo, Vincent A.,  
APPLICANT: Edinger, Shlomit R.,  
APPLICANT: Eisen, Andrew,  
APPLICANT: Ellerman, Karen,  
APPLICANT: Gangolli, Esha A.,  
APPLICANT: Gorman, Linda,  
APPLICANT: Gerlach, Valerie,  
APPLICANT: Ji, Weizhen,  
APPLICANT: Kekuda, Ramesh,  
APPLICANT: Khramtsov, Nikolai,  
APPLICANT: Li, Li,  
APPLICANT: Malyankar, Uriel M.,  
APPLICANT: MacDougall, John R.,  
APPLICANT: Mezes, Peter S.,  
APPLICANT: Miller, Charles E.,  
APPLICANT: Millet, Isabelle,  
APPLICANT: Ooi, Chean Eng,  
APPLICANT: Ort, Tatiana,  
APPLICANT: Padigaru, Muralidhara,  
APPLICANT: Patturajan, Meera,  
APPLICANT: Rastelli, Luca,  
APPLICANT: Rieger, Daniel K.,  
APPLICANT: Rothenberg, Mark E.,  
APPLICANT: Shenoy, Suresh G.,  
APPLICANT: Spaderna, Steven K.,  
APPLICANT: Spytek, Kimberley A.,  
APPLICANT: Taupier, Jr., Raymond J.,  
APPLICANT: Vernet, Corine A.M.,  
APPLICANT: Zerhusen, Bryan D.,  
APPLICANT: Zhong, Mei

TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

FILE REFERENCE: 21402-480C  
CURRENT APPLICATION NUMBER: US/10/287,226

CURRENT FILING DATE: 2002-11-04  
PRIOR FILING DATE: 2002-11-04  
PRIOR FILING DATE: 2001-11-30  
PRIOR FILING DATE: 2001-11-30  
PRIOR FILING DATE: 2002-02-04  
PRIOR FILING DATE: 2002-02-27  
PRIOR FILING DATE: 2002-03-13  
PRIOR FILING DATE: 2002-03-13  
PRIOR FILING DATE: 2002-08-20  
PRIOR FILING DATE: 2002-08-20  
PRIOR FILING DATE: 2001-11-30

PRIOR APPLICATION NUMBER: 60/354,409  
PRIOR FILING DATE: 2002-02-04  
PRIOR APPLICATION NUMBER: 60/364,227  
PRIOR FILING DATE: 2002-03-13  
PRIOR APPLICATION NUMBER: 60/334,027  
PRIOR FILING DATE: 2001-11-28  
PRIOR APPLICATION NUMBER: 60/331,641  
PRIOR FILING DATE: 2001-11-20  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 673  
SOFTWARE: CuraSeqList version 0.1  
SEQ ID NO 380  
LENGTH: 522  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-287-226-380

Query Match 95.4%; Score 527.5; DB 15; Length 522;

Best Local Similarity 77.9%; Pred. No. 1.7e-54;  
Matches 109; Conservative 0; Mismatches 0; Indels 31; Gaps 1;

Qy 1 SQIPASQETLVRPKPLLLKLLKSVGAQKQDTYTKK 36  
Dy 17 SQIPASQETLVRPKPLLLKLLKSVGAQKQDTYTKK 76  
Qy 37 -----VLFYLGQYIMTKRLYDEKQOHHIVYCSNDLLGDLFGVPFSFVKHHRKIYTMIR 89  
Dy 77 PKVLDLQVLFYLGQYIMTKRLYDEKQOHHIVYCSNDLLGDLFGVPFSFVKHHRKIYTMIR 136  
Qy 90 NLVVVNQOESSDSGTSVSEN 109  
Dy 137 NLVVVNQOESSDSGTSVSEN 156

## RESULT 13

US-10-287-226-382

Sequence 382, Application US/10287226  
Publication No. US20040086875A1

GENERAL INFORMATION:

APPLICANT: Agee, Michele L.,  
APPLICANT: Alsobrook, John P.,  
APPLICANT: Berghs, Constance,  
APPLICANT: Boldog, Ference,  
APPLICANT: Burgess, Catherine E.,  
APPLICANT: Chant, John S.,  
APPLICANT: Chaudhuri, Amitabha,  
APPLICANT: DiPippo, Vincent A.,  
APPLICANT: Edinger, Shlomit R.,  
APPLICANT: Eisen, Andrew,  
APPLICANT: Ellerman, Karen,  
APPLICANT: Gangolli, Esha A.,  
APPLICANT: Gorman, Linda,  
APPLICANT: Gerlach, Valerie,  
APPLICANT: Ji, Weizhen,  
APPLICANT: Kekuda, Ramesh,  
APPLICANT: Khramtsov, Nikolai,  
APPLICANT: Li, Li,  
APPLICANT: Malyankar, Uriel M.,  
APPLICANT: MacDougall, John R.,  
APPLICANT: Mezes, Peter S.,  
APPLICANT: Miller, Charles E.,  
APPLICANT: Millet, Isabelle,  
APPLICANT: Ooi, Chean Eng,  
APPLICANT: Ort, Tatiana,  
APPLICANT: Padigaru, Muralidhara,  
APPLICANT: Patturajan, Meera,  
APPLICANT: Rastelli, Luca,  
APPLICANT: Rieger, Daniel K.,  
APPLICANT: Rothenberg, Mark E.,  
APPLICANT: Shenoy, Suresh G.,  
APPLICANT: Spaderna, Steven K.,  
APPLICANT: Spytek, Kimberley A.,  
APPLICANT: Taupier, Jr., Raymond J.,

```

; APPLICANT: Vernet, Corine A.M.,
; APPLICANT: Zehrusen, Bryan D.,
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-480C
; CURRENT APPLICATION NUMBER: US/10/287,226
; CURRENT FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: 60/334,421
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/354,392
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/360,148
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: 60/364,000
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/404,821
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 60/334,526
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/354,409
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/364,227
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/334,027
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/331,641
; PRIOR FILING DATE: 2001-11-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 673
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 382
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-287-226-382

Query Match      95.4%; Score 527.5; DB 15; Length 522;
Best Local Similarity 77.9%; Pred. No. 1.7e-54;
Matches 109; Conservative 0; Mismatches 0; Indels 31; Gaps 1;

Qy 1 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKE----- 36
Db 17 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEWSFTMLPRLVWNSWAQICLPRP 76

Qy 37 -----VLFYLGQVIMTKRLYDEKQHIYVCSNDLLGLDGLFGVPSFVKHRKIYTMIR 89
Db 77 PKVLDQLVFLYLGQVIMTKRLYDEKQHIYVCSNDLLGLDGLFGVPSFVKHRKIYTMIR 136

Qy 90 NLVVVNQOESSDSGTSVSEN 109
Db 137 NLVVVNQOESSDSGTSVSEN 156

RESULT 14
US-09-956-425-6
; Sequence 6, Application US/09956425
; Patent No. US20020045192A1
; GENERAL INFORMATION:
; APPLICANT: Kriwacki, Richard
; APPLICANT: Bothner, Brian
; APPLICANT: Lewis, William
; TITLE OF INVENTION: A-f and Hdm2 Interaction Domains and Method of Use Thereof
; FILE REFERENCE: 1340/1/035
; CURRENT APPLICATION NUMBER: US/09/956,425
; CURRENT FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-956-425-6

```

```

Query Match      89.2%; Score 493.5; DB 9; Length 489;
Best Local Similarity 88.1%; Pred. No. 2e-50;
Matches 96; Conservative 7; Mismatches 3; Indels 3; Gaps 1;

Qy 1 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQVIMTKRLYDEKQHIYV 60
Db 17 SQIPASEQETLVVRPKPLLLKLLKSVGAQNDYTMKEIIFYIGQVIMTKRLYDEKQHIYV 76

Qy 61 CSNDLLGLDGLFGVPSFVKHRKIYTMIRNLVVVNQOESSDSGTSVSEN 109
Db 77 CSNDLLGLDGLFGVPSFVKHRKIYAMIRNLVAVSQO---DSGTSLSSES 122

RESULT 15
US-09-966-724-4
; Sequence 4, Application US/09966724
; Publication No. US20040170971A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G ST., N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/966,724
; FILING DATE: 01-Oct-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/044,619
; FILING DATE: 2001-10-01
; APPLICATION NUMBER: US 07/867,840
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.40148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-966-724-4

Query Match      89.2%; Score 493.5; DB 11; Length 489;
Best Local Similarity 88.1%; Pred. No. 2e-50;
Matches 96; Conservative 7; Mismatches 3; Indels 3; Gaps 1;

Qy 1 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQVIMTKRLYDEKQHIYV 60
Db 17 SQIPASEQETLVVRPKPLLLKLLKSVGAQNDYTMKEIIFYIGQVIMTKRLYDEKQHIYV 76

Qy 61 CSNDLLGLDGLFGVPSFVKHRKIYTMIRNLVVVNQOESSDSGTSVSEN 109
Db 77 CSNDLLGLDGLFGVPSFVKHRKIYAMIRNLVAVSQO---DSGTSLSSES 122

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Search completed: January 27, 2005, 18:23:04  
Job time : 75.4 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:45:30 ; Search time 80.8 Seconds  
(without alignments)  
483.929 Million cell updates/sec

Title: US-10-822-254-4

Perfect score: 521

Sequence: 1 SQPASEQYXVRPKPXLK.....NLVVNQSSDSGTSVSEN 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	506	97.1	284	2	AAR75494 Human dou
2	506	97.1	284	2	AAR75397 Human dou
3	506	97.1	491	2	AAR42175 Human MDM
4	506	97.1	491	2	AAR76696 Human MDM
5	506	97.1	491	2	AAR76696 Human MDM
6	506	97.1	491	2	AAR76696 Human MDM
7	506	97.1	491	2	AAR76696 Human MDM
8	506	97.1	491	2	AAR76696 Human MDM
9	506	97.1	491	2	AAR76696 Human MDM
10	506	97.1	491	2	AAR76696 Human MDM
11	506	97.1	491	2	AAR76696 Human MDM
12	506	97.1	491	2	AAR76696 Human MDM
13	506	97.1	491	2	AAR76696 Human MDM
14	506	97.1	491	2	AAR76696 Human MDM
15	506	97.1	491	2	AAR76696 Human MDM
16	506	97.1	491	2	AAR76696 Human MDM
17	506	97.1	491	2	AAR76696 Human MDM
18	506	97.1	491	2	AAR76696 Human MDM
19	506	97.1	491	2	AAR76696 Human MDM
20	506	97.1	491	2	AAR76696 Human MDM
21	506	97.1	491	2	AAR76696 Human MDM
22	506	97.1	491	2	AAR76696 Human MDM
23	506	97.1	491	2	AAR76696 Human MDM
24	506	97.1	491	2	AAR76696 Human MDM
25	506	97.1	491	2	AAR76696 Human MDM

26	506	97.1	491	8	ADQ19417	Adq19417 Human sof
27	506	97.1	1171	4	AAU32421	AAU32421 Novel hum
28	489.5	94.0	216	3	AAU08846	AAU08846 A human M
29	480.5	92.2	522	7	ADJ95152	ADJ95152 Novel NOV
30	480.5	92.2	522	7	ADJ95154	ADJ95154 Novel NOV
31	446.5	85.7	489	2	AAR42176	AAR42176 Murine MDM
32	446.5	85.7	489	2	AAR76697	AAR76697 Mouse MDM
33	446.5	85.7	489	2	AAW07888	AAW07888 Murine MDM
34	446.5	85.7	489	2	AAW15464	AAW15464 Murine MDM
35	446.5	85.7	489	2	AAW48242	AAW48242 Mouse MDM
36	446.5	85.7	489	2	AAW57246	AAW57246 Mouse MDM
37	446.5	85.7	489	2	AAW42997	AAW42997 Amino aci
38	446.5	85.7	489	2	AAW42972	AAW42972 Amino aci
39	446.5	85.7	489	2	AAW94305	AAW94305 Mouse MDM
40	446.5	85.7	489	5	AAE25914	AAE25914 Mouse dou
41	446.5	85.7	489	5	ABB57099	ABB57099 Mouse 1sc
42	446.5	85.7	489	5	AAO15375	AAO15375 Mouse Dm2
43	446.5	85.7	489	7	ADD21816	ADD21816 Mouse mdm
44	446.5	85.7	489	7	ADE61560	ADE61560 Rat Prote
45	322	61.8	227	2	AAR75495	AAR75495 Human dou

## ALIGNMENTS

RESULT 1  
AAR75494  
ID AAR75494 standard; protein; 284 AA.  
XX AAR75494;  
AC AAR75494;  
XX  
DT 02-FEB-1996 (first entry)  
XX  
DE Human double minute 2 (hdm-2) antibody-binding region fragment 1.  
XX  
KW Human double minute gene 2; hdm-2; antibody binding region; antigen;  
KW cancer; sarcoma; rhabdomyosarcoma; diagnosis; immunoassay.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Region 1..284  
FT /note= "amino acids 1-284 of hdm-2 gene product"  
XX  
XX DE4339533-A1.  
XX  
XX 14-JUN-1995.  
XX  
XX 19-NOV-1993; 93DE-04339533.  
XX  
XX 19-NOV-1993; 93DE-04339533.  
XX  
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
XX  
XX Zentgraf H, Klein R, Frey M, Martens R;  
XX WPI; 1995-216248/29.  
XX N-PSDB; AAQ92515.  
XX  
XX Detection of human double minute gene 2 (hdm-2) antibodies - by  
XX incubation with new hdm-2 or antibody-binding hdm-2 fragments; useful in  
XX the detection of specific cancers.  
XX  
XX Claim 11; Fig 1; 12pp; German.  
XX  
XX Fragments contg. amino acids 1-284, 58-284 and 58-491 of the hdm-2 (human  
XX double minute 2) gene product are claimed. The overlapping protein  
XX fragments contain binding regions for hdm-2- specific antibodies and are  
XX useful for identifying such antibodies in a claimed immunoassay method.  
XX The presence of anti-hdm-2 antibodies is diagnostic of certain forms of  
XX cancer, e.g. rhabdomyosarcoma  
XX  
XX Sequence 284 AA;

Query Match 97.1%; Score 506; DB 2; Length 284;  
 Best Local Similarity 93.6%; Pred. No. 1e-59;  
 Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 SQIPASEQETVVRPKPXLKLLKSVGAQKDTYTMKEVLXVYLGQYIMTKRLYDEKQOHIVX 60  
 DB 17 SQIPASEQETVVRPKPXLKLLKSVGAQKDTYTMKEVLXVYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDXLDGLFGVSPSVKHEHRKIYTMIXRNLVVVNQESSDSGTSVSEN 109  
 DB 77 CSNDLLGLDFGVSPSVKHEHRKIYTMIXRNLVVVNQESSDSGTSVSEN 125

RESULT 2  
 AAR75397  
 ID AAR75397 standard; protein; 284 AA.  
 AC AAR75397;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 25-JAN-1996 (first entry)  
 XX  
 DE Human double minute 2 (hdm-2) antibody-binding region fragment 1.  
 XX  
 KW Human double minute gene 2; hdm-2; antibody binding region; antigen;  
 KW cancer; sarcoma; rhabdomyosarcoma; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1..284  
 FT /note= "amino acids 1-284 of hdm-2 gene product"  
 XX  
 PN DE4345249-A1.  
 XX  
 XX 24-MAY-1995.  
 PD  
 PF 19-NOV-1993; 93DE-04345249.  
 XX  
 PR 19-NOV-1993; 93DE-04339533.  
 XX  
 XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
 PA  
 PI Zentgraf H, Klein R, Frey M, Martens R;  
 XX  
 XX WPI; 1995-195167/26.  
 DR N-PSDB; AAQ87261.  
 XX  
 PT New hdm-2 fragments contg. antibody binding region - used to detect  
 PT specific antibodies for diagnosis of cancers, also new DNA sequences  
 PT encoding them.  
 XX  
 PS Claim 2; Fig 1; 11pp; German.  
 XX  
 XX Fragments contg. amino acids 1-284, 58-284 and 58-491 of the hdm-2 (human  
 CC double minute 2) gene product are claimed. The overlapping protein  
 CC fragments contain binding regions for hdm-2- specific antibodies and are  
 CC useful for identifying such antibodies. The presence of anti-hdm-2  
 CC antibodies is diagnostic of certain forms of cancer, e.g.  
 CC rhabdomyosarcoma. (Updated on 25-MAR-2003 to correct PF field.)  
 XX  
 XX Sequence 284 AA;  
 SQ

Query Match 97.1%; Score 506; DB 2; Length 284;  
 Best Local Similarity 93.6%; Pred. No. 1e-59;  
 Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 SQIPASEQETVVRPKPXLKLLKSVGAQKDTYTMKEVLXVYLGQYIMTKRLYDEKQOHIVX 60  
 DB 17 SQIPASEQETVVRPKPXLKLLKSVGAQKDTYTMKEVLXVYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDXLDGLFGVSPSVKHEHRKIYTMIXRNLVVVNQESSDSGTSVSEN 109  
 DB 77 CSNDLLGLDFGVSPSVKHEHRKIYTMIXRNLVVVNQESSDSGTSVSEN 125

RESULT 4  
 AAR76696  
 ID AAR76696 standard; protein; 491 AA.

Db 77 CSNDLLGLDFGVSPSVKHEHRKIYTMIXRNLVVVNQESSDSGTSVSEN 125

RESULT 3  
 AAR42175  
 ID AAR42175 standard; protein; 491 AA.  
 AC AAR42175;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 05-MAY-1994 (first entry)  
 XX  
 DE Human MDM2.  
 XX  
 KW p53 gene; tumour suppressor gene; regulation; cellular proliferation;  
 KW cellular transformation; carcinoma; human; tumour; MDM2; inhibition;  
 KW gene amplification.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W09320238-A2.  
 XX  
 PD 14-OCT-1993.  
 XX  
 PF 07-APR-1993; 93WO-US003199.  
 XX  
 PR 07-APR-1992; 92US-00867840.  
 PR 23-JUN-1992; 92US-00903103.  
 XX  
 PA (UYJO) UNIV JOHNS HOPKINS.  
 XX  
 PI Burrell M, Hill DE, Kinzler KW, Vogelstein B;  
 XX  
 DR WPI; 1993-336944/42.  
 DR N-ESDB; AAQ49891.  
 XX  
 PT Diagnosing neoplasia from amplification of MDM2 gene - or elevated gene  
 PT expression, also new DNA, MDM2 protein, antibodies and treatment of  
 PT sarcoma by inhibiting MDM2 expression.  
 XX  
 PS Claim 19; Fig 1; 75pp; English.  
 XX  
 XX This sequence is encoded by the MDM2 gene. Amplification of the MDM2 gene  
 CC is diagnostic of neoplasia or the potential for neoplasia. The protein  
 CC encoded by this gene interacts with the product of the p53 gene. p53 is a  
 CC tumour suppressor gene and encodes a protein which appears to be a member  
 CC of a group of proteins which regulate normal cellular proliferation and  
 CC suppression of cellular transformation. Inactivation of the p53 gene has  
 CC been implicated in the formation, or progression of a wide variety of  
 CC carcinoma. Polypeptides containing at least amino acids 13-41 of p53, or  
 CC the DNA encoding these, may be used to inhibit the growth of tumour cells  
 CC containing MDM2 gene amplification. (Updated on 25-MAR-2003 to correct PN  
 CC field.)  
 XX  
 SQ Sequence 491 AA;  
 SQ

Query Match 97.1%; Score 506; DB 2; Length 491;  
 Best Local Similarity 93.6%; Pred. No. 2.2e-59;  
 Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 SQIPASEQETVVRPKPXLKLLKSVGAQKDTYTMKEVLXVYLGQYIMTKRLYDEKQOHIVX 60  
 DB 17 SQIPASEQETVVRPKPXLKLLKSVGAQKDTYTMKEVLXVYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDXLDGLFGVSPSVKHEHRKIYTMIXRNLVVVNQESSDSGTSVSEN 109  
 DB 77 CSNDLLGLDFGVSPSVKHEHRKIYTMIXRNLVVVNQESSDSGTSVSEN 125

RESULT 4  
 AAR76696  
 ID AAR76696 standard; protein; 491 AA.

XX AAR76696;  
 XX 16-OCT-2003 (revised)  
 DT 01-NOV-1995 (first entry)  
 XX Human MDM2 protein.  
 DE MDM2; sarcoma; diagnostic; DNA probe.  
 KW Homo sapiens; (cell line CaCo-2).  
 XX Homo sapiens; (cell line CaCo-2).  
 XX US5420263-A.  
 XX 30-MAY-1995.  
 XX 07-APR-1993; 93US-00044619.  
 XX 07-APR-1992; 92US-00867840.  
 PR 23-JUN-1992; 92US-00903103.  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 XX Vogelstein B, Kinzler KW;  
 XX WPI; 1995-206312/27.  
 DR N-PSDB; AAQ94589.  
 XX New human MDM2 cDNA - used to develop prods. for use in the diagnosis and treatment of tumours.  
 XX Claim 1; Col 23-26; 34pp; English.  
 XX The human MDM2 gene is genetically altered (i.e. amplified) in human tumour cells. The human MDM2 protein binds to human p53 and allows the cell to escape from p53-regulated growth. Detecting that the gene has become amplified or detecting increased gene product expression (using probes, proteins, antibodies and inhibitors) allows diagnosis and therapy of cancers such as colorectal carcinoma, lung cancer and chronic myelogenous leukaemia. (Updated on 16-OCT-2003 to standardise OS field)  
 XX Sequence 491 AA;  
 SQ  
 Query Match 97.1%; Score 506; DB 2; Length 491;  
 Best Local Similarity 93.6%; Pred. No. 2.2e-59;  
 Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 SQIPASEQETXVRPKPXLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQOHIVX 60  
 DB 17 SQIPASEQETLVRPKPXLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQOHIVY 76  
 QY 61 CSNDXLGDLFGVXSFVSVEHKKIYTMIXRNLVVNQESSDSGTSVSEN 109  
 DB 77 CSNDLLGDLFGVPSFVSVEHKKIYTMIXRNLVVNQESSDSGTSVSEN 125  
 RESULT 5  
 AA07887  
 ID AA07887 standard; protein; 491 AA.  
 XX AA07887;  
 XX 25-MAR-2003 (revised)  
 DT 28-JAN-1997 (first entry)  
 XX Human MDM-2, involved in tumour-development.  
 DE p53; MDM-2; binding-inhibitor; identification; tumour; cancer; neoplasia;  
 KW antibody fusion protein; therapy.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 XX Key Location/Qualifiers

FT Modified-site 166..169  
 FT /label= phosphorylation\_site  
 FT /note= "potential casein kinase II phosphorylation site"  
 FT Binding-site 181..185  
 FT /label= nuclear\_localisation\_signal  
 FT Modified-site 192..195  
 FT /label= phosphorylation\_site  
 FT /note= "potential casein kinase II phosphorylation site"  
 FT Domain 223..274  
 FT /label= acid\_activation\_domain  
 FT Modified-site 269..272  
 FT /label= phosphorylation\_site  
 FT /note= "potential casein kinase II phosphorylation site"  
 FT Modified-site 290..293  
 FT /label= phosphorylation\_site  
 FT /note= "potential casein kinase II phosphorylation site"  
 FT Domain 305..322  
 FT /label= metal\_binding\_site  
 FT Domain 461..478  
 FT /label= metal\_binding\_site  
 XX US5550023-A.  
 XX 27-AUG-1996.  
 XX 18-MAY-1994; 94US-00245500.  
 XX 07-APR-1992; 92US-00867840.  
 PR 23-JUN-1992; 92US-00903103.  
 PR 07-APR-1993; 93US-00044619.  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 XX Vogelstein B, Kinzler KW;  
 XX WPI; 1996-401591/40.  
 DR N-PSDB; AAT45151.  
 XX Identification of cpds. interfering with human MDM2/p53 binding - useful as therapeutic agents to treat human neoplastic cells.  
 XX Claim 26; Col 25-28; 36pp; English.  
 XX AA07887 represents human MDM-2 derived from a human colon carcinoma cell line, CaCo-2, cDNA library. The MDM-2 protein is used in a method for identifying compounds that interfere with the binding of p53 and MDM-2. In binding the p53 protein, the MDM-2 protein releases a cell from p53-regulated growth, allowing cancers to develop. Therefore compounds identified as interfering with the binding of MDM-2 to p53 are potentially useful in the treatment of human neoplastic cells. In the method pref. one or both of the proteins is a fusion protein esp. with an antibody or antibody fragment which aids separation and identification.  
 XX (Updated on 25-MAR-2003 to correct PF field.)  
 XX Sequence 491 AA;  
 SQ  
 Query Match 97.1%; Score 506; DB 2; Length 491;  
 Best Local Similarity 93.6%; Pred. No. 2.2e-59;  
 Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 SQIPASEQETXVRPKPXLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQOHIVX 60  
 DB 17 SQIPASEQETLVRPKPXLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQOHIVY 76  
 QY 61 CSNDXLGDLFGVXSFVSVEHKKIYTMIXRNLVVNQESSDSGTSVSEN 109  
 DB 77 CSNDLLGDLFGVPSFVSVEHKKIYTMIXRNLVVNQESSDSGTSVSEN 125  
 RESULT 6  
 AA07887  
 ID AA07887 standard; protein; 491 AA.  
 XX

```

AC AAW15463;
XX
XX 25-MAR-2003 (revised)
DT 18-JUN-1997 (first entry)
XX
XX Human MDM2.
XX
XX Human; MDM2 protein; antibody; detection; cancer; diagnosis;
KW p53-regulated growth.
XX
XX Homo sapiens.
OS
XX
XX US5618921-A.
XX
XX 08-APR-1997.
XX
XX 17-FEB-1995; 95US-00390479.
XX
XX 07-APR-1992; 92US-00867840.
PR 23-JUN-1992; 92US-00903103.
PR 07-APR-1993; 93US-00044619.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Vogelstein B, Kinzler KW, Burrell M, Hill DE;
XX
XX WPI; 1997-225474/20.
DR N-PSDB; AAT66410.
XX
XX Antibodies specific for human MDM2 protein - for diagnosis of cancer.
XX
XX Claim 1; Col 19-24; 35pp; English.
XX
XX This sequence represents the human MDM2 protein. Antibodies that
CC specifically bind to human MDM2 protein may be used for detecting
CC elevated expression of the MDM2 gene in a human tissue or body fluid
CC sample, esp. for cancer diagnosis. The antibodies may be used to
CC interfere with the binding of p53 to MDM2. Elevated levels of MDM2 appear
CC to sequester p53 and allow the cell to escape from p53-regulated growth.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 491 AA;
SQ
Query Match 97.1%; Score 506; DB 2; Length 491;
Best Local Similarity 93.6%; Pred. No. 2.2e-59;
Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 SQIPASEQETXVRPKPXLKLLKSVGAQKDTYTMKEVLXLYGQYIMTKRLYDEKQOHIVX 60
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLXLYGQYIMTKRLYDEKQOHIVY 76
QY 61 CSNDXLDGLFGVXSFVSKHEHKIYTMIXNLVNVNQESSDSGTSVSEN 109
Db 77 CSNDLLGDLFGVPSFVSKHEHKIYTMIXNLVNVNQESSDSGTSVSEN 125
XX
XX RESULT 7
XX AAW13380
XX ID AAW13380 standard; protein; 491 AA.
XX
XX AAW13380;
XX
XX 25-MAR-2003 (revised)
DT 05-JUN-1997 (first entry)
XX
XX Human MDM2 protein.
DE
XX
XX Human; MDM2; CaCo-2; colonic; carcinoma; probe; detection; amplification;
KW elevation; expression; diagnosis; neoplasia; neoplastic transformation;
KW sarcoma; colorectal; lung cancer; chronic myelogenous leukaemia.
XX
XX Homo sapiens.
OS
XX

```

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PN US5606044-A.
XX
XX 25-FEB-1997.
XX
XX 17-FEB-1995; 95US-00390546.
XX
XX 07-APR-1992; 92US-00867840.
PR 23-JUN-1992; 92US-00903103.
PR 07-APR-1993; 93US-00044619.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Kinzler KW, Vogelstein B, Hill DE, Burrell M;
XX
XX WPI; 1997-153623/14.
DR N-PSDB; AAT62065.
XX
XX Detection of amplification of human MDM2 gene - useful for diagnosis of
PT neoplasia or potential neoplastic transformation.
XX
XX Example 1; Col 21-24; 35pp; English.
XX
XX The present sequence is the human MDM2 protein, the cDNA for which was
CC isolated from a human CaCo-2 colonic carcinoma cell cDNA library using a
CC murine MDM2 cDNA probe. The MDM2 cDNA can be used as a probe to detect
CC the amplification or elevated expression of a human MDM2 gene, which is
CC diagnostic of neoplasia or the potential for neoplastic transformation,
CC useful for the detection of, e.g. sarcomas, colorectal carcinoma, lung
CC cancer and chronic myelogenous leukaemia. (Updated on 25-MAR-2003 to
CC correct PF field.)
XX
XX Sequence 491 AA;
SQ
Query Match 97.1%; Score 506; DB 2; Length 491;
Best Local Similarity 93.6%; Pred. No. 2.2e-59;
Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 SQIPASEQETXVRPKPXLKLLKSVGAQKDTYTMKEVLXLYGQYIMTKRLYDEKQOHIVX 60
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLXLYGQYIMTKRLYDEKQOHIVY 76
QY 61 CSNDXLDGLFGVXSFVSKHEHKIYTMIXNLVNVNQESSDSGTSVSEN 109
Db 77 CSNDLLGDLFGVPSFVSKHEHKIYTMIXNLVNVNQESSDSGTSVSEN 125
XX
XX RESULT 8
XX AAW13600
XX ID AAW13600 standard; protein; 491 AA.
XX
XX AAW13600;
XX
XX 16-JAN-1998 (first entry)
DT
DE Murine double minute 2 protein sequence.
XX
XX Mouse; Mdm2; murine double minute; phosphoprotein; binding; modulation;
KW tumour suppressor; p53; oncogene; cell cycle arrest; p107; antagonist;
KW inhibition; transcription factor; adenocarcinoma; colon; cancer; breast;
KW lung; stomach; myeloid leukaemia; lymphoma; hyperproliferative;
KW restenosis.
XX
XX Mus musculus.
OS
XX
XX WO9709343-A2.
PN
XX
XX 13-MAR-1997.
PD
XX
XX 02-SEP-1996; 96WO-FR001340.
PF
XX
XX 04-SEP-1995; 95FR-00010331.
PR
XX
XX (RHON ) RHONE POULENC RORER SA.
PA

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CC WITH THE BINDING OF MOMZ AND P33. SINCE MOMZ IS OVEREXPRESSED IN

CC cells and since binding of MDM2 to p53 appears to allow tumour cells to  
 CC escape from p53-regulated growth, compounds that inhibit such binding  
 CC would be useful as anti-cancer agents

SQ Sequence 491 AA;

Query Match 97.1%; Score 506; DB 2; Length 491;

Best Local Similarity 93.6%; Pred. No. 2.2e-59;  
 Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 SQIPASEQETXVRPKPXLKLLKLSVGAQKDTYTMKEVLXLYLQYIMTKELYDEKQOHIVX 60  
 |||||  
 DB 17 SQIPASEQETLVRPKPLLLKLLKLSVGAQKDTYTMKEVLXLYLQYIMTKELYDEKQOHIVY 76  
 |||||  
 QY 61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVNQESSDSTSVSEN 109  
 |||||  
 DB 77 CSNDLLGDLFGVPFSVKEHRKIYTMIXRNLVVNQESSDSTSVSEN 125  
 |||||

#### RESULT 13

AAW94304  
 ID AAW94304 standard; protein; 491 AA.

XX AC AAW94304;

XX DT 13-APR-1999 (first entry)

XX DE Human MDM2.

XX KW Human; MDM2; p53; tumorigenesis; growth regulation; diagnosis;

XX KW malignant fibrous histiocytoma; MFH; liposarcoma.

XX OS Homo sapiens.

XX PN US5858976-A.

XX PD 12-JAN-1999.

XX PF 14-FEB-1997; 97US-00801718.

XX PR 07-APR-1992; 92US-00867840.

XX PR 23-JUN-1992; 92US-00903103.

XX PR 07-APR-1993; 93US-00044619.

XX PR 17-FEB-1995; 95US-00390515.

XX PA (UYGO ) UNIV JOHNS HOPKINS.

XX PI Kinzler KW, Vogelstein B;

XX DR WPI; 1999-152105/13.

XX DR N-PSDB; AAX03947.

XX PT Inhibiting growth of tumour cells having MDM2 gene amplification - with  
 PT MDM2-binding p53 fragment.

PS Claim 1; Col 23-28; 41pp; English.

XX The present invention describes: (1) a method for inhibiting the growth  
 CC of tumour cells which contain a human MDM2 gene amplification, comprising  
 CC administering to the cells a DNA molecule that expresses a polypeptide  
 CC consisting of a portion of p53 i.e. amino acids 13-41 of the 64 amino  
 CC acid sequence given in AAW94303, the polypeptide being capable of binding  
 CC to human MDM2 (the present sequence); (2) a method as in (1) where the  
 CC polypeptide lacks the homo-oligomerisation domain of p53; and (3) a  
 CC method as in (1) where the polypeptide lacks amino acids 138-393 of p53.  
 CC The method is useful for treating the following tumour types which have a  
 CC MDM2 gene amplification: M-7 malignant fibrous histiocytoma (MFH), M-20  
 CC MFH, L-9 liposarcoma, KL7 liposarcoma, KL28 liposarcoma, KL30  
 CC liposarcoma, and OSA-CL MFH

SQ Sequence 491 AA;

Query Match 97.1%; Score 506; DB 2; Length 491;

Best Local Similarity 93.6%; Pred. No. 2.2e-59;  
 Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 SQIPASEQETXVRPKPXLKLLKLSVGAQKDTYTMKEVLXLYLQYIMTKELYDEKQOHIVX 60  
 |||||  
 DB 17 SQIPASEQETLVRPKPLLLKLLKLSVGAQKDTYTMKEVLXLYLQYIMTKELYDEKQOHIVY 76  
 |||||

QY 61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVNQESSDSTSVSEN 109  
 |||||

DB 77 CSNDLLGDLFGVPFSVKEHRKIYTMIXRNLVVNQESSDSTSVSEN 125  
 |||||

#### RESULT 14

AA956567

ID AA956567 standard; protein; 491 AA.

XX AC AA956567;

XX DT 12-SEP-2000 (first entry)

XX DE MDM2 oncoprotein.

XX KW hEST2; telomerase; catalytic subunit; reverse transcriptase; life-span;

XX KW retinoblastoma; p53; tumour suppressor; inhibitor; arteriosclerosis;

XX KW proliferation; immortal; tumour therapy; macular degeneration; activator;

XX KW INK4; MDM2; oncoprotein.

XX OS Homo sapiens.

XX PN WO200031238-A2.

XX PD 02-JUN-2000.

XX PF 24-NOV-1999; 99WO-US027907.

XX PR 25-NOV-1998; 98US-0109891P.

XX PR 17-FEB-1999; 99US-0120549P.

XX PA (GENE-) GENETICA INC.

XX PI Hannon GJ, Beach DH;

XX DR WPI; 2000-400055/34.

XX DR N-PSDB; AAA29389.

XX PT New method for increasing the proliferative capacity of cell lines  
 PT comprises administering agents reversibly activating telomerase activity  
 PT and reversibly inactivating Rb/INK4 and/or p53 pathways useful in  
 PT treating age related diseases.

PS Claim 5; Page 120; 123pp; English.

XX The invention concerns methods and reagents for extending the life-span,  
 CC e.g. the number of mitotic divisions, of a cell. The method relies on  
 CC activation of a telomerase activity and inhibition of one or both of a  
 CC retinoblastoma (Rb)/INK4 pathway or a p53 pathway. Phosphorylation of Rb  
 CC by cyclin-dependent kinases, cdk4 and cdk6, releases the cells into the  
 CC division cycle. Binding of INK4 family members, e.g. the tumour  
 CC suppressor p16INK4a, inhibits kinase activity and results in growth  
 CC arrest. Rb inactivators can selectively and reversibly inactivate an  
 CC Rb/INK4 pathway, especially an Rb/p16INK4a pathway. The oncoprotein MDM2  
 CC is a cellular inhibitor of Rb/E2F function and the p53 tumour suppressor  
 CC and can also be used in the methods. Other molecules which can be used  
 CC include cdk4 or cdk6 mutants. In particular, a cdk4 mutant is one which  
 CC differs from at one or more of residues K22, R24, H95 and/or D97.  
 CC Additional constructs include a papilloma virus E7 protein, or other  
 CC viral oncoprotein which bypasses Rb and/or p53. Antisense constructs of  
 CC the Rb and p16INK4a genes may also be used. The methods are useful for  
 CC increasing the proliferative capacity of cells. The cells are  
 CC subsequently of use in pharmaceutical and cosmetic preparations used to  
 CC treat conditions related to (premature) ageing, e.g. macular degeneration  
 CC and arteriosclerosis. The cells can also be used to replace tumour cell  
 CC lines in vitro and for studies on biochemical and physiological aspects

CC of growth and differentiation. Long lived (immortal) cells could also be  
 CC of use in the production of normal or genetically engineered  
 CC biotechnology products  
 XX  
 SQ Sequence 491 AA;

Query Match 97.1%; Score 506; DB 3; Length 491;  
 Best Local Similarity 93.6%; Pred. No. 2.2e-59;  
 Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVX 60  
 DB 17 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDXLGDLFGVXSFVSKHRKIYTMIXRNLVVNNQOESSDSGTSVSEN 109  
 DB 77 CSNDLLGDLFGVPFSFVSKHRKIYTMIXRNLVVNNQOESSDSGTSVSEN 125

RESULT 15  
 AAB48284  
 ID AAB48284 standard; protein; 491 AA.

XX AC AAB48284;

DT 02-APR-2001 (first entry)

XX DE Human MDM2 protein.

XX KW S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; 2F;  
 KW CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;  
 KW Bad; Bcl-2; tumour; cytostatic.

XX OS Homo sapiens.

XX PN WO200075184-A1.

XX PD 14-DEC-2000.

XX PF 05-JUN-2000; 2000WO-US015449.

XX PR 04-JUN-1999; 99US-0137494P.

XX PA (UYIA ) UNIV YALE.

XX PI Zhang H, Tsvetkov LM, Kondo T;

DR WP1; 2001-061703/07.

DR N-PSDB; AAC84596.

XX PT Modulating polypeptide levels in a cell, diagnosing and treating tumor,  
 PT involves altering levels of proteins such as S-phase kinase associated  
 PT proteins 1, 2 and cullin/CDC53 proteins.

XX PS Claim 5; Page 93-95; 162pp; English.

XX CC The invention relates to methods of altering the polypeptide levels in a  
 CC cell, using proteins selected from S-phase kinase associated proteins 1  
 CC and 2 (SKP1, SKP2), SKP2-like proteins (2F) and CUL-1 (a member of the  
 CC cullin/ CDC53 family of proteins). The method is useful for altering the  
 CC level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2  
 CC polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for  
 CC detecting tumours, and in monitoring tumor treatment in a mammal. Agents  
 CC that modulate interactions between SKP and target proteins are useful for  
 CC treating tumours

XX SQ Sequence 491 AA;

Query Match 97.1%; Score 506; DB 4; Length 491;  
 Best Local Similarity 93.6%; Pred. No. 2.2e-59;  
 Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVX 60

DB 17 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76  
 QY 61 CSNDXLGDLFGVXSFVSKHRKIYTMIXRNLVVNNQOESSDSGTSVSEN 109  
 DB 77 CSNDLLGDLFGVPFSFVSKHRKIYTMIXRNLVVNNQOESSDSGTSVSEN 125

Search completed: January 27, 2005, 18:06:15  
 Job time : 80.8 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:52:56 ; Search time 19.8 Seconds  
(without alignments)  
529.678 Million cell updates/sec

Title: US-10-822-254-4  
Perfect score: 521  
Sequence: 1 SQIPASBQETVVRPKPXLK.....NLVVNQESSDSGTSVSEN 109

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: Pirl.\*  
2: Pirl.\*  
3: Pirl.\*  
4: Pirl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	506	97.1	491	1 S24354	p53-binding protein
2	446.5	85.7	489	2 S15349	mdm2 protein - mou
3	266.5	51.2	489	2 I91955	MDM2-like p53-bind
4	71	13.6	838	2 I45557	eyeless, long form
5	68	13.1	683	2 T38254	serine/threonine-s
6	68	13.1	685	1 SXBPT4	NAD+-protein ADP-r
7	68	13.1	698	1 S31630	NAD+-protein ADP-r
8	66.5	12.8	425	2 T50184	mammalian swi/snf
9	66.5	12.8	517	2 S32169	hypothetical prote
10	66	12.7	181	2 S75415	probable ribosomal
11	66	12.7	187	2 S70186	21k protein - Shig
12	65	12.5	331	2 B84938	flagellar motor sw
13	64.5	12.4	380	2 T32112	hypothetical prote
14	64.5	12.4	447	2 I64002	sodium-translocati
15	64.5	12.4	467	2 T25848	hypothetical prote
16	64.5	12.4	525	2 T15185	hypothetical prote
17	64.5	12.4	286	2 B37743	exodeoxyribonuclea
18	64	12.3	413	2 B83950	processing protein
19	63.5	12.2	709	2 E64213	DNA topoisomerase
20	63.5	12.2	337	1 ZHBPG4	gene H protein - p
21	63	12.1	456	2 AG3471	beta-alanine-pyruv
22	63	12.1	456	2 AG3471	denosylmethionine-
23	62.5	12.0	451	2 P93747	probable phytochro
24	62.5	12.0	636	2 H96666	exodeoxyribonuclea
25	62	11.9	261	2 H71680	methenyltetrahydro
26	62	11.9	316	2 F69491	DNA primase TC0175
27	62	11.9	600	2 H81733	Ras guanine nucleo
28	62	11.9	1333	2 A37488	Ras guanine nucleo
29	62	11.9	1336	2 S25716	Ras guanine nucleo

## RESULT 1

S24354

p53-binding protein mdm2 - human

N:Alternate names: mdm-2 oncogene; mouse double minute 2, splice form A

N:Contains: p53-binding protein mdm2, splice form A

C:Species: Homo sapiens (man)

C>Date: 17-Mar-2000 #sequence revision 17-Mar-2000 #text\_change 17-Mar-2000

C:Accession: S24354; S57338; G02026

R:Oliner, J.D.; Kinzler, K.W.; Meltzer, P.S.; George, D.L.; Vogelstein, B.

Nature 358, 80-83, 1992

A:Title: Amplification of a gene encoding a p53-associated protein in human sarcomas.

A:Reference number: S24354; MUID:92310576; PMID:1614537

A:Accession: S24354

A:Molecule type: mRNA

A:Residues: 1-491 <OLI>

A:Cross-references: EMBL:Z12020; NID:G35211; PIDN:CAA78055.1; PID:G35212

R:Zauberman, A.; Flusberg, D.; Haupt, Y.; Barak, Y.; Oren, M.

Nucleic Acids Res. 23, 2584-2592, 1995

A:Title: A functional p53-responsive intronic promoter is contained within the human mdm

A:Reference number: S57338; MUID:95380270; PMID:7651818

A:Accession: S57338

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-16, 'p', 18-24 <ZAU>

A:Cross-references: EMBL:U28935; NID:G904033; PIDN:AAA82237.1; PID:G904034

R:Lunec, J

submitted to the EMBL Data Library, August 1995

A:Description: Multiple alternate spliced mdm2 transcripts with loss of p53 binding doma

A:Reference number: G09070

A:Accession: G02026

A:Status: translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-27,223-491 <LIN>

A:Cross-references: EMBL:U33199; NID:G992676; PIDN:AAA75514.1; PID:G992677

A:Experimental source: splice form A

C:Genetics:

A:Gene: GDB:MDM2

A:Cross-references: GDB:250456; OMIM:164785

A:Map position: 12q14.3-12q15

C:Superfamily: human p53-binding protein mdm2

C:Keywords: alternative splicing; oncogene; phosphoprotein

F:1-491/Product: p53-binding protein mdm-2 #status predicted <MAT1>

F:1-27,223-491/Product: p53-binding protein mdm-2, splice form A #status predicted <MAT2>

Query Match 97.1%; Score 506; DB 1; Length 491;

Best Local Similarity 93.6%; Pred. No. 8.3e-50;

Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 SQIPASBQETVVRPKPXLKLLKLSVGAQKDTYTKMKVLXVLYGOYIMTKRLYDEKQOHLVX 60

Db 17 SQIPASBQETVVRPKPXLKLLKLSVGAQKDTYTKMKVLFYLGQYIMTKRLYDEKQOHLVY 76



```
Db 551 PASKVPESIRSKLQLLKHFKSYMGONLSKAVQDSFEPKPKNSTNTMLFMQHILRT----- 606
Qy 52 DEKQOHIVKCSNDXLGDLFGVXSFSVKEHRK-IYTMIXRNLVNVNQ 97
Db 607 --RQAIMFRLSN-----GIFQFNFLDRKRVISSTARKIIVLDKE 644

RESULT 6
SBPT4
NAD+-protein ADP-ribosyltransferase (EC 2.4.2.-) precursor - phase T4
C:Species: phase T4
A:Note: host Escherichia coli
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C:Accession: J00096
R:Hilse, D.; Koch, T.; Rueger, W.
Nucleic Acids Res. 17, 6731, 1989
A:Title: Nucleotide sequence of the alt gene of bacteriophage T4.
A:Reference number: J00096; MUID:89386005; PMID:2506526
A:Accession: J00096
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-685 <HL>
A:Cross-references: UNIPROT:P12726
C:Comment: This enzyme catalyzes the ADP-ribosylation of one of the two alpha-subunits of
C:Genetics:
A:Gene: alt
C:Superfamily: phage T4 NAD-protein ADP-ribosyltransferase
C:Keywords: glycosyltransferase; pentosyltransferase
F:7-685/Product: NAD-protein ADP-ribosyltransferase #status predicted <MAT>

Query Match 13.1%; Score 68; DB 1; Length 685;
Best Local Similarity 27.0%; Pred. No. 11;
Matches 27; Conservative 22; Mismatches 37; Indels 14; Gaps 6;

Qy 18 LLKLLKS--VGAQKDYTMKEVLXYL---GOYIMTKRL--YDEKQOHI-VKCSNDXLGDL 69
Db 111 MLRLKSKTAGAQRQIQVIADRLIRSRGGRYLLKELWDYDKKYAYILIHRRKNVSLDI 170
Qy 70 FGVSFSVKEHRKIYTMIXRNLVNVNQESSDSGTSVSEN 109
Db 171 PGVPEISTELFTKVESKVGDD--VYINK----DTGAQVTKN 204

RESULT 7
S31630
NAD+-protein ADP-ribosyltransferase (EC 2.4.2.-) precursor - phase T2
C:Species: phase T2
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S31630
R:Koch, T.; Rueger, W.
A:Description: The ADP-ribosyltransferase of bacteriophages T2, T4 and T6: Sequencing of
A:Reference number: S31630
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-698 <KOC>
A:Cross-references: UNIPROT:Q38424; EMBL:X69893; NID:g15187; PIDN:CAA49517.1; PID:g15188
C:Superfamily: phage T4 NAD-protein ADP-ribosyltransferase
C:Keywords: glycosyltransferase; NAD; pentosyltransferase

Query Match 13.1%; Score 68; DB 1; Length 698;
Best Local Similarity 27.0%; Pred. No. 12;
Matches 27; Conservative 22; Mismatches 37; Indels 14; Gaps 6;

Qy 18 LLKLLKS--VGAQKDYTMKEVLXYL---GOYIMTKRL--YDEKQOHI-VKCSNDXLGDL 69
Db 112 MLRLKSKTAGAQRQIQVIADRLIRSRGGRYLLKELWDYDKKYAYILIHRRKNVSLDI 171
Qy 70 FGVSFSVKEHRKIYTMIXRNLVNVNQESSDSGTSVSEN 109
Db 172 PGVPEISTELFTKVESKVGDD--VYINK----DTGAQVTKN 205
```

## RESULT 8

S31714  
NAD+-protein ADP-ribosyltransferase (EC 2.4.2.-) precursor - phase T6  
C:Species: phase T6  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: S31714  
R:Koch, T.; Rueger, W.  
A:Description: The ADP-ribosyltransferase of bacteriophages T2, T4 and T6: Sequencing of  
submitted to the EMBL Data Library, December 1992  
A:Reference number: S31630  
A:Accession: S31714  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-698 <KOC>  
A:Cross-references: UNIPROT:Q38433; EMBL:X69894; NID:g15422; PIDN:CAA49518.1; PID:g15423  
C:Superfamily: phage T4 NAD-protein ADP-ribosyltransferase  
C:Keywords: glycosyltransferase; NAD; pentosyltransferase

Query Match 13.1%; Score 68; DB 1; Length 698;

Best Local Similarity 27.0%; Pred. No. 12;  
Matches 27; Conservative 22; Mismatches 37; Indels 14; Gaps 6;

Qy 18 LLKLLKS--VGAQKDYTMKEVLXYL---GOYIMTKRL--YDEKQOHI-VKCSNDXLGDL 69  
Db 112 MLRLKSKTAGAQRQIQVIADRLIRSRGGRYLLKELWDYDKKYAYILIHRRKNVSLDI 171

Qy 70 FGVSFSVKEHRKIYTMIXRNLVNVNQESSDSGTSVSEN 109

Db 172 PGVPEISTELFTKVESKVGDD--VYINK----DTGAQVTKN 205

## RESULT 9

T50184  
mammalian swi/snf complex 60 kda subunit homolog [imported] - fission yeast (Schizosacch  
C:Species: Schizosaccharomyces pombe  
C:Date: 09-Jun-2000 #sequence\_revision 09-Jun-2000 #text\_change 09-Jul-2004  
C:Accession: T50184  
R:Badcock, K.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, February 2000  
A:Reference number: Z25044  
A:Accession: T50184  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-425 <BAD>  
A:Cross-references: UNIPROT:Q9PTS3; EMBL:AL138854; PIDN:CAB72235.1; GSPDB:GNO00066; SPDB  
A:Experimental source: strain 972h(-); cosmid C23G3  
C:Genetics:  
A:Gene: SPDB:SPAC23G3.10C  
A:Map position: 1

Query Match 12.8%; Score 66.5; DB 2; Length 425;  
Best Local Similarity 36.8%; Pred. No. 9.7;  
Matches 14; Conservative 9; Mismatches 14; Indels 1; Gaps 1;

Qy 33 TMKEVLXYLGOYIMTKRLYDEKQOHI-VKCSNDXLGDLF 70

Db 222 TRPDIVSLWQYIKFRLQDMEEKRLINC-DKALRDLF 258

## RESULT 10

S32169  
hypothetical protein 2 - Myxococcus xanthus  
C:Species: Myxococcus xanthus  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S32169; S67952  
R:Botella, J.; Murillo, F.; Ruiz-vazquez, R.  
submitted to the EMBL Data Library, March 1993  
A:Description: Nucleotide and deduced protein sequences of a carotenoid gene cluster in  
A:Reference number: S32168  
A:Accession: S32169  
A:Molecule type: DNA



A;Accession: S70186  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-187 <UCH>  
A;Cross-references: UNIPROT:Q52996; EMBL:D26468; NID:g992954; PIDN:BAA05481.1; PID:d1006  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1994

Query Match 12.7%; Score 66; DB 2; Length 187;  
Best Local Similarity 21.6%; Pred.No. 4.3;  
Matches 21; Conservative 15; Mismatches 33; Indels 28; Gaps 3;

Qy 23 KSVGAQQTYYMKVILXYLGQYIMTKRLYDEKQQ-----HIVKCSNDXL 66  
:|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
Db 40 RSARAGRDDWLKEILL-----RVYDENHQVVAVRKVWHQLLRGIRVARTVARL 89

Qy 67 GDLFVGUKSFVSEHRKIYTMIXRNLVVVNQESSDSG 103  
:|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
Db 90 MAVMGLA--GVLRGGKVHTTVSRKAAGDRVNRHQG 124

RESULT 13  
B84938  
flagellar motor switch protein flig [imported] - Buchnera sp. (strain APS)  
C;Species: Buchnera sp.  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 24-Aug-2001  
C;Accession: B84938  
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.  
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp.  
A;Reference number: A84930; MUID:20445173; PMID:10993077  
A;Accession: B84938  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-331 <STO>  
A;Cross-references: GB:AP000398; GSPDB:GN00144  
A;Experimental source: strain APS  
C;Genetics:  
A;Gene: flig; BU074  
C;Superfamily: flagellar switch protein flig

Query Match 12.5%; Score 65; DB 2; Length 331;  
Best Local Similarity 27.1%; Pred.No. 11;  
Matches 23; Conservative 16; Mismatches 28; Indels 18; Gaps 3;

Qy 18 LLKLL-KSVAQKDQTYTMKEVLYXGLGYIMTKRLYDEKQHIVKCSNDXLGDLFVGXSFS 76  
:|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
Db 77 LIKMLTKALGEKKGTSLTKEALETRNARI CIKALNYMKAKQVAFLLD----- 123

Qy 77 VKEHKIYTMIXRNLVVVNQESSD 101  
||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
Db 124 -KEHPQIIITVI---LICLNKNQSAR 144

RESULT 14  
T32112  
hypothetical protein F59E11.8 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T32112  
R;Bradshaw, H.  
submitted to the EMBL Data Library, July 1997  
A;Description: The sequence of C. elegans cosmid F59E11.  
A;Reference number: Z21124  
A;Accession: T32112  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-380 <BRA>  
A;Cross-references: UNIPROT:Q22556; EMBL:AF016695; PIDN:AAB66222.1; GSPDB:GN00023; CESP:  
A;Experimental source: strain Bristol N2; clone F59E11  
C;Genetics:  
A;Gene: CESP:F59E11.8  
A;Map position: 5  
A;Introns: 72/2; 92/1; 118/3; 191/3; 223/3; 345/3



Query Match 12.4%; Score 64.5; DB 2; Length 380;  
Best Local Similarity 28.7%; Pred. No. 14;  
Matches 27; Conservative 18; Mismatches 24; Indels 25; Gaps 6;  
QY 1 SOIPASEQETKVRPKPXLKLL-----KSVGAQKDTYTMKEVLXVLGQYIMTKRLY 51  
DB 296 NKIGGSMQKTYT-----LLNLADNLHEYYVEQDKATRYSLTKILKISQY---KTLM 348  
QY 52 DEKQOHVXCSNDXLGDLFGVKSFSVK-EHRKIY 84  
DB 349 EEKRR-----TEVLGDVFG--APRVKWSHSEIP 374

RESULT 15  
I64002  
sodium-translocating NADH dehydrogenase (ubiquinone) (EC 1.6.5.-) alpha chain HI0164 [sl  
C;Species: Haemophilus influenzae  
C;Date: 18-Aug-1995 #sequence\_revision 02-Sep-2000 #text\_change 09-Jul-2004  
C;Accession: I64002; A64003  
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.  
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.  
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.  
Science 269, 496-512, 1995  
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,  
A.;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A;Reference number: A64000; MUID:95350630; PMID:7542800  
A;Accession: I64002  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-447 <TIGR>  
A;Cross-references: UNIPROT:P43955; GB:L42023; TIGR:HI0164; GB:U32702; NID:g1573118; PID  
A;Note: the sequence is revised in GenBank entry U32702, PID:g1573122  
C;Superfamily: Vibrio alginolyticus sodium-translocating NADH dehydrogenase (ubiquinone)  
C;Keywords: oxidoreductase

Query Match 12.4%; Score 64.5; DB 2; Length 447;  
Best Local Similarity 25.0%; Pred. No. 17;  
Matches 28; Conservative 16; Mismatches 41; Indels 27; Gaps 5;  
QY 1 SOIPASEQ-----TXVRPKPXL---LKLKSVGAQKDTY--TMKEVLXVLGQYIMTK 48  
DB 198 SNIFTADLENLQIHDFTGVHPAGLVGTHIFIDPVGIOKTVWHINYQDVIA-VGKLFTTG 256  
QY 49 RLYDEKQOHVXCSNDXLGDLFGVKSFSVKEHRKIYTMIXRNLVVVNQCESS 100  
DB 257 ELYSER-----VISLAGPQVKEPRLVRTTIGANLSQLTQNELS 294

Search completed: January 27, 2005, 18:15:09  
Job time : 20.8 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 27, 2005, 17:51:46 ; Search time 84.6 Seconds  
(without alignments)  
741.322 Million cell updates/sec

Title: US-10-822-254-4

Perfect score: 521

Sequence: 1 SQIPASQETXVRPKPKLLK.....NLVVNQESSDSGTSVSEN 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	506	97.1	166	Q8NDW2	Q8ndw2 homo sapien
2	506	97.1	195	Q96DS4	Q96ds4 homo sapien
3	506	97.1	243	Q8TE47	Q8te47 homo sapien
4	506	97.1	491	1 MDM2 HUMAN	Q00987 homo sapien
5	506	97.1	491	2 AAP35922	Aap35922 homo sapi
6	506	97.1	491	2 AAH67077	Aah67077 homo sapi
7	494	94.8	487	1 MDM2 CANFA	P36950 canis fami
8	494	94.8	487	2 Q9GMZ6	Q9gmz6 canis fami
9	494	94.8	491	1 MDM2 HORSE	P56951 equus cabal
10	491	94.2	491	2 Q7YRZ8	Q7yrz8 felis silve
11	456	87.5	436	2 Q8WYJ2	Q8wyj2 homo sapien
12	446.5	85.7	489	1 MDM2 MOUSE	P33804 mus musculu
13	446.5	85.7	489	2 Q91XK7	Q91xk7 m mus muscu
14	429	82.3	118	2 Q8WYJ3	Q8wyj3 homo sapien
15	428.5	82.2	466	1 MDM2 MESAU	Q60524 mesocricetu
16	393	75.4	325	2 Q9PVL2	Q9pvl2 gallus gall
17	368	70.6	173	2 Q8TE46	Q8te46 homo sapien
18	344	66.0	473	1 MDM2 XENLA	P36273 xenopus lae
19	344	66.0	473	2 Q6GMB5	Q6gmb5 xenopus lae
20	343	65.8	482	2 Q6P3Q9	Q6p3q9 xenopus tro
21	343	65.8	482	2 AAH63898	Aah63898 xenopus t
22	314.5	60.4	105	2 Q8NDW0	Q8ndw0 homo sapien
23	290	55.7	426	2 Q8GK41	Q8gk41 canis fami
24	280.5	53.8	445	1 MDM2 BRARE	O42354 brachydanio
25	280.5	53.8	445	2 AA00198	Aa00198 brachydanio
26	270	51.8	491	2 Q7ZUW7	Q7zuw7 brachydanio
27	266.5	51.2	489	1 MDM4 MOUSE	Q35618 mus musculu
28	263.5	50.6	489	2 Q8CYG1	Q8cyg1 m mus muscu
29	263	50.5	475	2 Q7ZYI3	Q7zyi3 xenopus lae
30	262.5	50.4	446	2 Q8WYJ1	Q8wyj1 homo sapien
31	257	49.3	490	2 Q99L86	Q99l86 mus musculu

32	251.5	48.3	134	2 Q6PHL8	Q6phl8 xenopus lae
33	251.5	48.3	134	2 AAH56503	Aah56503 xenopus l
34	241	46.3	153	2 Q6MZR7	Q6mzr7 homo sapien
35	241	46.3	153	2 CAE45961	Ca45961 homo sapi
36	241	46.3	490	2 AAH67299	Aah67299 homo sapi
37	239	45.9	490	1 MDM4 HUMAN	O15151 homo sapien
38	206	39.5	69	2 Q86WA4	Q86wa4 homo sapien
39	199	38.2	66	2 Q96DS3	Q96ds3 homo sapien
40	196	37.6	70	2 Q86WA3	Q86wa3 homo sapien
41	184	35.3	95	2 Q96DS1	Q96ds1 homo sapien
42	168	32.2	159	2 Q96DS0	Q96ds0 homo sapien
43	167	32.1	70	2 Q8NDW1	Q8ndw1 homo sapien
44	166	31.9	60	2 Q96DS5	Q96ds5 homo sapien
45	166	31.9	130	2 Q9H4C3	Q9h4c3 homo sapien

#### ALIGNMENTS

##### RESULT 1

Q8NDW2 ID Q8NDW2 PRELIMINARY; PRT; 166 AA.  
AC Q8NDW2;  
DT 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE P53-binding protein.  
GN Name=MDM2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bartel F., Pinkert D., Kappeler M., Rache M., Schmidt H., Taubert H.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ491698; CAD36959.1; -.  
DR HSSP; Q9UNT8; 1YCR.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR InterPro; IPR010984; MDM2.  
DR InterPro; IPR003121; SWIB\_MDM2.  
DR Pfam; PF02201; SWIB; 1.  
SQ SEQUENCE 166 AA; 18900 MW; FA6B5BA18E85040D CRC64;

Query Match 97.1%; Score 506; DB 2; Length 166;

Best Local Similarity 93.6%; Pred. No. 2.4e-50;

Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 SQIPASQETXVRPKPKLLKLLKSVGAQKQDTYTWKVLXLYLQYIMTKRLYDEKQOHIVX 60

Db 17 SQIPASQETILVRPKPLLLKLLKSVGAQKQDTYTWKVLFLYLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDXLGDLFGVXSFVKEHKIYTMIXRNLVVNVNQESSDSGTSVSEN 109

Db 77 CSNDLLGDLFGVPSFVKEHKRIYTMIXRNLVVNVNQESSDSGTSVSEN 125

##### RESULT 2

Q96DS4 ID Q96DS4 PRELIMINARY; PRT; 195 AA.  
AC Q96DS4;  
DT 01-DEC-2001 (TReMBLrel. 19, Created)  
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE MDM2 variant FB26.  
GN Name=MDM2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Rhabdomyosarcoma tumor;

RA Bartel F., Taylor A.C., Taubert H., Harris L.C.;  
RL Submitted (MAY-2001) to the ENBL/GenBank/DBJ databases.  
DR EMBL; AF385323; AAL13243.1; -  
DR HSSP; Q9UMT8; 1YCR.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR InterPro; IPR010984; MDM2.  
DR InterPro; IPR003121; SWIB\_MDM2.  
DR Pfam; PF02201; SWIB; 1.  
SQ SEQUENCE 195 AA; 22161 MW; 4987AE567DB12DSD CRC64;  
  
Query Match 97.1%; Score 506; DB 2; Length 195;  
Best Local Similarity 93.6%; Pred. No. 2.9e-50;  
Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
  
Qy 1 SQIPASEQETVRPKPXLKLLKSVGAQKDTYTMKEVLXLYGQYIMTKRLYDEKQOHIVX 60  
Dy 17 SQIPASEQETVRPKPXLKLLKSVGAQKDTYTMKEVLXLYGQYIMTKRLYDEKQOHIVY 76  
  
Qy 61 CSNDXGLGDLFGVKSFSVKEHRKIYTMIXRNLVVNVNQSSDSGTSVSEN 109  
Dy 77 CSNDLLGLDGLFGVPSFVKEHRKIYTMIXRNLVVNVNQSSDSGTSVSEN 125  
  
RESULT 3  
Q8TE47 PRELIMINARY; PRT; 243 AA.  
ID Q8TE47  
AC Q8TE47;  
DT 01-JUN-2002 (TRENBLrel. 21, Created)  
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)  
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
DE MDM2 isoform KB9 protein.  
GN Name=MDM2 isoform KB9;  
OS Homo sapiens (Human).  
OC Eukaryota; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM MDM2).  
RC TISSUE=Lymphocytes;  
RA Bartel F., Pinkert D., Kappler M., Bache M., Schmidt H., Taubert H.;  
RL Submitted (FEB-2002) to the ENBL/GenBank/DBJ databases.  
DR EMBL; AJ430612; CAD23251.1; -  
DR HSSP; Q9UMT8; 1YCR.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.  
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.  
DR GO; GO:0008270; F:zinc ion binding; IEA.  
DR GO; GO:0016567; P:protein ubiquitination; IEA.  
DR InterPro; IPR010984; MDM2.  
DR InterPro; IPR003121; SWIB\_MDM2.  
DR InterPro; IPR001841; Znf\_Fing.  
DR Pfam; PF02201; SWIB; 1.  
DR SMART; SM00184; RING; 1.  
DR PROSITE; PS50089; ZF\_RING\_2; 1.  
SQ SEQUENCE 243 AA; 27317 MW; 9EB5D0142CF185A2 CRC64;  
  
Query Match 97.1%; Score 506; DB 2; Length 243;  
Best Local Similarity 93.6%; Pred. No. 3.6e-50;  
Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
  
Qy 1 SQIPASEQETVRPKPXLKLLKSVGAQKDTYTMKEVLXLYGQYIMTKRLYDEKQOHIVX 60  
Dy 17 SQIPASEQETVRPKPXLKLLKSVGAQKDTYTMKEVLXLYGQYIMTKRLYDEKQOHIVY 76  
  
Qy 61 CSNDXGLGDLFGVKSFSVKEHRKIYTMIXRNLVVNVNQSSDSGTSVSEN 109  
Dy 77 CSNDLLGLDGLFGVPSFVKEHRKIYTMIXRNLVVNVNQSSDSGTSVSEN 125  
  
RESULT 4  
MDM2 HUMAN STANDARD; PRT; 491 AA.  
ID MDM2 HUMAN  
AC Q00987; Q13226; Q13297; Q13298; Q13299; Q13300; Q13301; Q9UGI3;

AC Q9UMT8;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Hdm2).  
GN Name=MDM2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM MDM2).  
RC TISSUE=Ovarian carcinoma;  
RA Oliner J.D., Kinzler K.W., Meltzer P.S., George D.L., Vogelstein B.;  
RT "Amplification of a gene encoding a p53-associated protein in human sarcomas.";  
RL Nature 358:80-83 (1992).  
[2]  
RP SEQUENCE FROM N.A. (ISOFORMS MDM2-A; -B; -C; -D AND -E).  
RC TISSUE=Ovarian carcinoma;  
RA Sigalas I., Calvert A.H., Anderson J.J., Neal D.E., Lunec J.;  
RT "Alternatively spliced mdm2 transcripts with loss of p53 binding domain sequences: transforming ability and frequent detection in human cancer.";  
RL Nat. Med. 2:912-917 (1996).  
[3]  
RP SEQUENCE FROM N.A. (ISOFORM MDM2-ALPHA).  
RC TISSUE=Ovarian carcinoma;  
RA Veldhoen N., Metcalfe S., Milner J.;  
RT "A novel exon within the mdm2 gene modulates translation initiation in vitro and disrupts the p53-binding domain of mdm2 protein.";  
RL Oncogene 18:7026-7033 (1999).  
[4]  
RP SEQUENCE FROM N.A. (ISOFORM MDM2).  
RC TISSUE=Muscle;  
RA Rieder M.J., Livingston R.J., Braun A.C., Montoya M.A., Chung M.-W., Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;  
RT "NIHES-SNPs, environmental genome project, NIHES ES15478, Department of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";  
RL Submitted (JUL-2002) to the ENBL/GenBank/DBJ databases.  
[5]  
RP SEQUENCE FROM N.A. (ISOFORM MDM2).  
RC TISSUE=Muscle;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
[6]  
RP SEQUENCE OF 6-491 FROM N.A. (ISOFORM MDM2-A1).  
RA Liang H., Atkins H., Abdel-Fattah R., Saeun R., Lunec J.;  
RT "Genomic organisation of the human MDM2 oncogene and relationship to its alternatively spliced mRNA's.";  
RL Submitted (NOV-1999) to the ENBL/GenBank/DBJ databases.  
[7]

RP SEQUENCE OF 1-24 FROM N.A.  
RA MEDLINE=95380270; PubMed=7651818;  
RX Zauberman A., Flusberg D., Haupt Y., Barak Y., Oren M.;  
RA "A functional p53-responsive intronic promoter is contained within the  
RT human mdm2 gene";  
RL Nucleic Acids Res. 23:2584-2592(1995).  
RN [8]  
RP SEQUENCE OF 1-9 FROM N.A.  
RX MEDLINE=97413643; PubMed=9270029;  
RA Landers J.E., Cassel S.L., George D.L.;  
RX "Translational enhancement of mdm2 oncogene expression in human tumor  
RT cells containing a stabilized wild-type p53 protein.";  
RL Cancer Res. 57:3562-3568(1997).  
RN [9]  
RP SEQUENCE OF 301-481 FROM N.A.  
RX MEDLINE=20542019; PubMed=11087894;  
RA Taubert H., Kappler M., Meyer A., Bartel F., Schlott T.,  
RX Lautenschlaeger C., Bache M., Schmidt H., Wuerl P.;  
RT "A MboII polymorphism in exon 11 of the human MDM2 gene occurring in  
RL normal blood donors and in soft tissue sarcoma patients: an indication  
RN for an increased cancer susceptibility?";  
RX Mutat. Res. 456:39-44(2000).  
RN [10]  
RP MUTAGENESIS OF CVS-464.  
RX MEDLINE=98111004; PubMed=9450543;  
RA Honda R., Tanaka H., Yasuda H.;  
RX "Oncoprotein MDM2 is a ubiquitin ligase E3 for tumor suppressor p53.";  
RL FEBS Lett. 420:25-27(1997).  
RN [11]  
RP MUTAGENESIS OF CVS-449.  
RX MEDLINE=20190101; PubMed=10723139;  
RA Honda R., Yasuda H.;  
RX "Activity of MDM2, a ubiquitin ligase, toward p53 or itself is  
RT dependent on the RING finger domain of the ligase.";  
RL Oncogene 19:1473-1476(2000).  
RN [12]  
RP MUTAGENESIS.  
RX MEDLINE=20187618; PubMed=10722742;  
RA Fang S., Jensen J.P., Ludwig R.L., Vousden K.H., Weissman A.M.;  
RX "Mdm2 is a RING finger-dependent ubiquitin protein ligase for itself  
RT and p53";  
RL J. Biol. Chem. 275:8945-8951(2000).  
RN [13]  
RP MUTAGENESIS OF CVS-441 AND CVS-478.  
RX MEDLINE=20076498; PubMed=10608892;  
RA Sharp D.A., Kratowicz S.A., Sank M.J., George D.L.;  
RX "Stabilization of the MDM2 oncoprotein by interaction with the  
RT structurally related MDMX protein.";  
RL J. Biol. Chem. 274:38189-38196(1999).  
RN [14]  
RP NUCLEOLAR LOCALIZATION SIGNAL.  
RX MEDLINE=20173879; PubMed=10707090;  
RA Lohrum M.A.E., Ashcroft M., Kubbutat M.H.G., Vousden K.H.;  
RX "Identification of a cryptic nucleolar-localization signal in MDM2.";  
RL Nat. Cell Biol. 2:179-181(2000).  
RN [15]  
RP PHOSPHORYLATION BY ATM.  
RX MEDLINE=20079591; PubMed=10611322;  
RA Khosravi R., Maya R., Gottlieb T., Oren M., Shiloh Y., Shkedy D.;  
RX "Rapid ATM-dependent phosphorylation of MDM2 precedes p53 accumulation  
RT in response to DNA damage.";  
RL Proc. Natl. Acad. Sci. U.S.A. 96:14973-14977(1999).  
RN [16]  
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 25-109 IN COMPLEX WITH P53.  
RX MEDLINE=97081050; PubMed=8875929;  
RA Kussie P.H., Gorina S., Marechal V., Elenbaas B., Moreau J.,  
RX Levine A.J., Pavletich N.P.;  
RT "Structure of the MDM2 oncoprotein bound to the p53 tumor suppressor  
RL transactivation domain.";  
RL Science 274:948-953(1996).  
CC -1- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and  
CC apoptosis by binding its transcriptional activation domain.  
CC Functions as a ubiquitin ligase E3, in the presence of E1 and E2,

CC toward p53 and itself. Permits the nuclear export of p53 and  
CC targets it for proteasome-mediated proteolysis.  
CC -1- COFACTOR: Zinc is required for ubiquitin ligase E3 activity.  
CC -1- SUBUNIT: Binds p53, p73, ARF(p14), ribosomal protein L5 and  
CC specifically to RNA. Can interact also with retinoblastoma protein  
CC (RB). E1A-associated protein EP300 and the E2F1 transcription  
CC factor.  
CC -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed  
CC predominantly in the nucleoplasm. Interaction with ARF(p14)  
CC results in the localization of both proteins to the nucleolus. The  
CC nucleolar localization signals in both ARF(p14) and MDM2 may be  
CC necessary to allow efficient nucleolar localization of both  
CC proteins.  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=8;  
CC Name=Mdm2;  
CC IsoId=Q00987-1; Sequence=Displayed;  
CC Name=Mdm2-A;  
CC IsoId=Q00987-2; Sequence=VSP\_003208;  
CC Name=Mdm2-A1;  
CC IsoId=Q00987-3; Sequence=VSP\_003208, VSP\_003214;  
CC Name=Mdm2-B;  
CC IsoId=Q00987-4; Sequence=VSP\_003209;  
CC Name=Mdm2-C;  
CC IsoId=Q00987-5; Sequence=VSP\_003211;  
CC Name=Mdm2-D;  
CC IsoId=Q00987-6; Sequence=VSP\_003210;  
CC Name=Mdm2-E;  
CC IsoId=Q00987-7; Sequence=VSP\_003212, VSP\_003213;  
CC Name=Mdm2-alpha;  
CC IsoId=Q00987-8; Sequence=VSP\_003207;  
CC -1- TISSUE SPECIFICITY: Ubiquitous. Isoforms MDM2-A, -B, -C, -D and -E  
CC are observed in a range of human cancers but absent in normal  
CC tissues.  
CC -1- INDUCTION: By DNA damage.  
CC -1- DOMAIN: Region I is sufficient for binding p53 and inhibiting its  
CC G1 arrest and apoptosis functions. It also binds p73 and E2F1.  
CC Region II contains most of a central acidic region required for  
CC interaction with ribosomal protein L5 and a putative C4-type zinc  
CC finger. The RING finger domain which coordinates two molecules of  
CC zinc interacts specifically with RNA whether or not zinc is  
CC present and mediates the hetero-oligomerization with MDM4. It is  
CC also essential for its ubiquitin ligase E3 activity toward p53 and  
CC itself.  
CC -1- PTM: Phosphorylated in response to ionizing radiation in an ATM-  
CC dependent manner.  
CC -1- DISEASE: Seems to be amplified in certain tumors (including soft  
CC tissue sarcomas, osteosarcomas and gliomas). A higher frequency of  
CC splice variants lacking p53 binding domain sequences was found in  
CC late-stage and high-grade ovarian and bladder carcinomas. Four of  
CC the splice variants show loss of p53 binding.  
CC -1- MISCELLANEOUS: MDM2 RING finger mutations that failed to  
CC  
Query Match 97.1%; Score 506; DB 1; Length 491;  
Best Local Similarity 93.6%; Pred. No. 8e-50;  
Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
Qy 1 SQIPASQETXVRPKPXLKLLKSVGAQKDYTKWEVLXVYLGQYIMTKRLYDEKQHVX 60  
Db 17 SQIPASQETLVPRKPLLLKLLKSVGAQKDYTKWEVLXVYLGQYIMTKRLYDEKQHVY 76  
Qy 61 CSNDXLGDLFGVXSPSVKHEHRKIYTMIXRNLVVNVNQSSDSTGTSVSEN 109  
Db 77 CSNDLIGDLFGVPSFVKHEHRKIYTMIVRNLVVNVNQSSDSTGTSVSEN 125  
RESULT 5  
AAP35922  
ID AAP35922 PRELIMINARY; PRT; 491 AA.  
AC AAP35922  
DT 02-MAR-2004 (TRENBLrel. 27, Created)  
DT 02-MAR-2004 (TRENBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TRENBLrel. 27, Last annotation update)

Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse).  
 DE Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RA Kainine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,  
 RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,  
 RA Phelan M., Farmer A.;  
 RA "Cloning of human full-length cDNAs in BD Creator(TM) System Donor  
 RT vector";  
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BT007258; AAP35922.1; --  
 SQ SEQUENCE 491 AA; 55232 MW; F37CE163876BC983 CRC64;  
 Query Match 97.1%; Score 506; DB 2; Length 491;  
 Best Local Similarity 93.6%; Pred. No. 8e-50;  
 Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 SQIPASEQETVVRPKPKLLKLLKSVGAQKDTYTMKEVLVYLQYIMTKRLYDEKQOHVX 60  
 DB 17 SQIPASEQETVVRPKPKLLKLLKSVGAQKDTYTMKEVLVYLQYIMTKRLYDEKQOHVY 76  
 QY 61 CSNDXGLDGLFGVPSFVKHRIKTYMTXRNLVVNNQESSDSTSVSEN 109  
 DB 77 CSNDLLGLDGLFGVPSFVKHRIKTYMTXRNLVVNNQESSDSTSVSEN 125  
 RESULT 6  
 AAH67077 PRELIMINARY; PRT; 491 AA.  
 AC AAH67077;  
 DT 14-APR-2004 (TrEMBLrel. 27, Created)  
 DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Muscle;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshlyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Hellon E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalek U., Smalish D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Muscle;  
 RA Strausberg R.;  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC067077; AAH67077.1; --  
 KW Hypothetical protein.

SQ SEQUENCE 491 AA; 55232 MW; F37CE163876BC983 CRC64;  
 Query Match 97.1%; Score 506; DB 2; Length 491;  
 Best Local Similarity 93.6%; Pred. No. 8e-50;  
 Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 SQIPASEQETVVRPKPKLLKLLKSVGAQKDTYTMKEVLVYLQYIMTKRLYDEKQOHVX 60  
 DB 17 SQIPASEQETVVRPKPKLLKLLKSVGAQKDTYTMKEVLVYLQYIMTKRLYDEKQOHVY 76  
 QY 61 CSNDXGLDGLFGVPSFVKHRIKTYMTXRNLVVNNQESSDSTSVSEN 109  
 DB 77 CSNDLLGLDGLFGVPSFVKHRIKTYMTXRNLVVNNQESSDSTSVSEN 125  
 RESULT 7  
 MDM2\_CANFA STANDARD; PRT; 487 AA.  
 ID MDM2\_CANFA  
 AC P56950; Q95KNS;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein  
 DE Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Cdm2).  
 GN Name=MDM2;  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 NCBI\_TaxID=9615;  
 [1]  
 RN SEQUENCE OF 1-484 FROM N.A.  
 RP MEDLINE=20218866; PubMed=10754200;  
 RA Nasir L., Burr P.D., McFarlane S.T., Gault E., Thompson H.,  
 RA Argyle D.J.;  
 RT "Cloning, sequence analysis and expression of the cDNAs encoding the  
 RT canine and equine homologues of the mouse double minute 2 (mdm2)  
 RT proto-oncogene";  
 RL Cancer Lett. 152:9-13(2000).  
 [2]  
 RN SEQUENCE FROM N.A. (ISOFORMS MDM2 AND MDM2-ALPHA).  
 RP MEDLINE=20065171; PubMed=10597303;  
 RA Veldhoen N., Metcalfe S., Milner J.;  
 RT "A novel exon within the mdm2 gene modulates translation initiation in  
 RT vitro and disrupts the p53-binding domain of mdm2 protein";  
 RL Oncogene 18:7026-7033(1999).  
 CC -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and  
 CC apoptosis by binding its transcriptional activation domain.  
 CC Functions as a ubiquitin ligase E3, in the presence of E1 and E2,  
 CC toward p53 and itself. Permits the nuclear export of p53 and  
 CC targets it for proteasome-mediated proteolysis (By similarity).  
 CC -!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity (By  
 CC similarity).  
 CC -!- SUBUNIT: Binds p53, p73, ARF(p14), ribosomal protein L5 and  
 CC specifically to RNA. Can interact also with retinoblastoma protein  
 CC (Rb), E1A-associated protein EP300 and the E2F1 transcription  
 CC factor (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed  
 CC predominantly in the nucleoplasm (By similarity).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=Mdm2;  
 CC IsoId=P56950-1; Sequence=Displayed;  
 CC Name=Mdm2-alpha;  
 CC IsoId=P56950-2; Sequence=VSP\_003206;  
 CC -!- TISSUE SPECIFICITY: Isoform Mdm2-alpha is present in lymphoid and  
 CC testicular tissues.  
 CC -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its  
 CC G1 arrest and apoptosis functions. It also binds p73 and E2F1.  
 CC Region II contains most of a central acidic region required for  
 CC interaction with ribosomal protein L5 and a putative C4-type zinc  
 CC finger. The RING finger domain which coordinates two molecules of  
 CC zinc interacts specifically with RNA whether or not zinc is  
 CC present and mediates the hetero-oligomerization with MDM4. It is

OX	NCBI_TaxID=9615;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Liver;
RA	Setouchi A., Tsujimoto H.;
RL	Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AB031276; BAB11975.1; -.
DR	HSSP; Q9UMT8; IYCR.
DR	GO; GO:0005730; C:nucleolus; ISS.
DR	GO; GO:0005654; C:nucleoplasm; ISS.
DR	GO; GO:0017163; F:negative regulator of basal transcription a. . . ; ISS.
DR	GO; GO:0005515; F:protein binding; ISS.
DR	GO; GO:0000122; P:negative regulation of transcription from P. . . ; ISS.
DR	InterPro; IPRO010984; MDM2.
DR	InterPro; IPRO03131; SWIB MDM2.
DR	InterPro; IPRO01876; Znf_RanGDP.
DR	InterPro; IPRO01841; Znf_ring.
DR	Pfam; PF02201; SWIB; 1.
DR	Pfam; PF00641; zf-RanBP; 1.
DR	SMART; SMO0184; RING; 1.
DR	PROSITE; PS01358; ZF_RANBP2_1; 1.
DR	PROSITE; PS01199; ZF_RANBP2_2; 1.
DR	PROSITE; PSS0089; ZF_RING_2; 1.
SQ	SEQUENCE 487 AA; 54724 MW; 34FC5CC6A18D7744 CRC64;

Query Match 94.8%; Score 494; DB 2; Length 487;  
 Best Local Similarity 90.8%; Pred. No. 1.9e-48;  
 Matches 99; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy	1	SQIPASEOETVVPKPKXLLKLKLSGAQKDVTMKVEVLXVLGYIMTKRLYDEKQHIVX	60
Dd	17	SQIPASEOETLVVRPKPELLLKLSGAQKDVTMKVEIFYLGQYIMTKRLYDEKQHIVY	76
Qy	61	CNSDLGLGDFGVXSFSVKERKIYTIYRNLVVNVOESDSGTSVSEN	109
Dd	77	CNSDLLGLGDFGVDSFSVKERKIYTIYRNLVVNVOHPSDSGTSVSEN	125

RESULT 9  
MDM2 HORSE

ID	MDM2_HORSE	STANDARD;	PRT;	491 AA.
AC	P5695I;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DE	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein			
DE	Mdm2) (oncoprotein Mdm2) (Double minute 2 protein) (Edm2).			
GN	Names=MDM2;			
OS	Equus caballus (Horse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.			
OX	NCBI_TaxID=9796;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RL	MEDLINE=20218866; PubMed=10754200;			
RA	Nasir L., Burr P.D., McFarlane S.T., Gault E., Thompson H.,			
RA	Argyle D.J.			
RT	"Cloning, sequence analysis and expression of the cDNAs encoding the			
RT	canine and equine homologues of the mouse double minute 2 (mdm2)			
RT	proto-oncogene."			
RL	Cancer Lett. 152:9-13(2000).			
CC	-1- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and			
CC	apoptosis by binding its transcriptional activation domain.			
CC	Functions as a ubiquitin ligase E3, in the presence of E1 and E2,			
CC	toward p53 and itself. Permits the nuclear export of p53 and			
CC	targets it for proteasome-mediated proteolysis (By similarity).			
CC	-1- COFACTOR: Zinc is required for ubiquitin ligase E3 activity (By			
CC	similarity).			
CC	-1- SUBUNIT: Binds p53, p73, ARF(p14), ribosomal protein L5 and			
CC	specifically to RNA. Can interact also with retinoblastoma protein			
CC	(RB), E1A-associated protein EFP00 and the E2F1 transcription			
CC	factor (By similarity).			
CC	-1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed			

CC predominantly in the nucleoplasm (By similarity).

CC -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its

CC G1 arrest and apoptosis functions. It also binds p73 and E2F1.

CC Region II contains most of a central acidic region required for

CC interaction with ribosomal protein L5 and a putative C4-type zinc

CC finger. The RING finger domain which coordinates two molecules of

CC zinc interacts specifically with RNA whether or not zinc is

CC present and mediates the hetero-oligomerization with MDM4. It is

CC also essential for its ubiquitin ligase E3 activity toward p53 and

CC itself (By similarity).

CC -!- SIMILARITY: Belongs to the MDM2 / MDM4 family.

CC -!- SIMILARITY: Contains 1 RanBP2-type zinc finger.

CC -!- SIMILARITY: Contains 1 RING-type zinc finger.

CC -!- SIMILARITY: Contains 1 SWIB domain.

CC -----

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CC use by non-profit institutions as long as its content is in no way

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----

CC EMBL; AF121140; AAF28866.1; -.

CC HSSP; Q9UMT8; 1YCR.

CC InterPro; IPR010984; MDM2.

CC InterPro; IPR003121; SWIB.

CC InterPro; IPR001876; Znf\_RanGDP.

CC InterPro; IPR001841; Znf\_ring.

CC Pfam; PF02201; SWIB; 1.

CC Pfam; PF00641; zf-RanBP; 1.

CC SMART; SM00184; RING; 1.

CC PROSITE; PS01358; ZF\_RANBP2\_1; 1.

CC PROSITE; PS00519; ZF\_RANBP2\_2; 1.

CC PROSITE; PS00516; ZF\_RING\_1; FALSE\_NEG.

CC PROSITE; PS00089; ZF\_RING\_2; 1.

CC Ligase; Metal-binding; Nuclear protein; Ubl conjugation pathway; Zinc;

CC Zinc-finger.

CC FT DOMAIN 27 107 SWIB.

CC FT DOMAIN 179 185 Nuclear localization signal (Potential).

CC FT DOMAIN 190 202 Nuclear export signal.

CC FT DOMAIN 210 304 ARF-binding.

CC FT DOMAIN 210 215 Poly-Ser.

CC FT DOMAIN 242 331 Region II.

CC FT DOMAIN 243 301 Asp/Glu-rich (acidic).

CC FT DOMAIN 299 328 RanBP2-type.

CC FT ZN\_FING 438 479 RING-type.

CC FT ZN\_FING 466 473 Nucleolar localization signal

CC FT DOMAIN (Potential).

CC SQ SEQUENCE 491 AA; 55279 MW; 641E033D5C1DEC39 CRC64;

Query Match 94.8%; Score 494; DB 1; Length 491;

Best Local Similarity 90.8%; Pred. No. 2e-48; Mismatches 8; Indels 0; Gaps 0;

Matches 99; Conservative 2;

AC Q7YRZ8 PRELIMINARY; PRT; 491 AA.

DT 01-OCT-2003 (TrEMBLrel. 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Double minute 2 protein MDM2.

GN Name=mdm2;

QY 1 SQIPASEQETVVRPKPXLKLLKSVGAQKQTYTWMKEVLXLYLGQYIMTKRLYDEKQOHIVX 60

DB 17 SQIPASEQETLVVRPKPXLKLLKSVGAQKQTYTWMKEVLXLYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDKLGDLFGVKSFSVKEHRKIYTMIXRNLVVWVQSSDSGTSVSEN 109

DB 77 CSNDLLGDLFGVPSFVKEHRKIYTMIXRNLVVWVQSPSPSGTSVSEN 125

RESULT 10

QYRZ8

ID Q7YRZ8 PRELIMINARY; PRT; 491 AA.

AC Q7YRZ8

DT 01-OCT-2003 (TrEMBLrel. 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Double minute 2 protein MDM2.

GN Name=mdm2;

OS Felis silvestris catus (Cat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.

OX NCBI\_TaxID=9685;

EN [1]

RP SEQUENCE FROM N.A.

RA Miki R., Okuda M., Ma Z., Inokuma H., Onishi T.;

RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB099709; BAC78209.1; -.

DR GO; GO:0005730; C:nucleolus; ISS.

DR GO; GO:0005654; C:nucleoplasm; ISS.

DR GO; GO:0017163; F:negative regulator of basal transcription a. . .; ISS.

DR GO; GO:0005515; F:protein binding; ISS.

DR GO; GO:000122; P:negative regulation of transcription from P. . .; ISS.

DR InterPro; IPR003121; SWIB MDM2.

DR InterPro; IPR001876; Znf\_RanGDP.

DR InterPro; IPR001841; Znf\_ring.

DR Pfam; PF02201; SWIB; 1.

DR Pfam; PF00641; zf-RanBP; 1.

DR SMART; SM00184; RING; 1.

DR PROSITE; PS01358; ZF\_RANBP2\_1; 1.

DR PROSITE; PS00199; ZF\_RANBP2\_2; 1.

DR PROSITE; PS00089; ZF\_RING\_2; 1.

SQ SEQUENCE 491 AA; 55433 MW; D93E25D638E88934 CRC64;

Query Match 94.2%; Score 491; DB 2; Length 491;

Best Local Similarity 89.9%; Pred. No. 4.3e-48;

Matches 98; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 SQIPASEQETVVRPKPXLKLLKSVGAQKQTYTWMKEVLXLYLGQYIMTKRLYDEKQOHIVX 60

DB 17 SQIPASEQETLVVRPKPXLKLLKSVGAQKQTYTWMKEVLXLYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDKLGDLFGVKSFSVKEHRKIYTMIXRNLVVWVQSSDSGTSVSEN 109

DB 77 CSNDLLGDLFGVPSFVKEHRKIYTMIXRNLVVWVQHPSPSGTSVSEN 125

RESULT 11

Q8WYJ2

ID Q8WYJ2 PRELIMINARY; PRT; 436 AA.

AC Q8WYJ2;

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE MDM2 protein.

GN Name=MDM2;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

EN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21248713; PubMed=11351297;

RA Tamborini E., Della Torre G., Lavarino C., Azzarelli A.,

RA Carpinelli P., Pierotti M.A., Pilotti S.;

RT "Analysis of the molecular species generated by MDM2 gene

RT amplification in liposarcomas.";

RL Int. J. Cancer 92:790-796(2001).

DR EMBL; AF092844; AAL40179.1; -.

DR HSSP; Q9UMT8; 1YCR.

DR GO; GO:0005730; C:nucleolus; ISS.

DR GO; GO:0005654; C:nucleoplasm; ISS.

DR GO; GO:0017163; F:negative regulator of basal transcription a. . .; ISS.

DR GO; GO:0005515; F:protein binding; ISS.

DR GO; GO:000122; P:negative regulation of transcription from P. . .; ISS.

DR InterPro; IPR010984; MDM2.

DR InterPro; IPR003121; SWIB MDM2.

DR InterPro; IPR001876; Znf\_RanGDP.

DR Pfam; PF02201; SWIB; 1.

DR Pfam; PF00641; zf-RanBP; 1.

DR SMART; SM00184; RING; 1.



```

DR PROSITE: PS01358; ZF_RANBP2_1; 1.
DR PROSITE: PS01199; ZF_RANBP2_2; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
SQ SEQUENCE 436 AA; 49248 MW; 3CBF55E98BC4203A CRC64;

Query Match 87.5%; Score 456; DB 2; Length 436;
Best Local Similarity 87.6%; Pred No. 4.3e-44;
Matches 92; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

Qy 1 SQIPASEQETVVRPKPKXLLKLLKSGAQAQDTYTKMEVLYLQGYIMTKRLYDEKQOHIVX 60
Dy 17 SQIPASEQETVVRPKPKXLLKLLKSGAQAQDTYTKMEVLYLQGYIMTKRLYDEKQOHIVY 76
Qy 61 CSNDXLDGLFGVKSFSVKEHKRIYTMIXRNVLVNVNQESSDSGTS 105
Dy 77 CSNDLLGDLFGVKSFSVKEHKRIYTMIXRNVLVNVNQESSDSGLS 121

RESULT 12
MDM2_MOUSE
ID MDM2_MOUSE STANDARD; PRT; 489 AA.
AC P23804; Q61040; Q64330;
DT 01-NOV-1991 (Rel. 20, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein
DE Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein).
GN Name=Mdm2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A. (ISOFORM MDM2-P90).
RA Fakhrazadeh S.S., Trusko S.P., George D.L.;
RX MEDLINE=91224107; PubMed=2026149;
RT "Tumorigenic potential associated with enhanced expression of a gene
RT that is amplified in a mouse tumor cell line.";
RL EMBO J. 10:1565-1569(1991).
[2]
SEQUENCE FROM N.A. (ISOFORM MDM2-P90).
RC STRAIN=129/SV;
RX MEDLINE=97074674; PubMed=8917101;
RA Jones S.N., Ansari-Lari M.A., Hancock A.R., Jones W.J., Gibbs R.A.,
RA Donehower L.A., Bradley A.;
RT "Genomic organization of the mouse double minute 2 gene.";
RL Gene 175:209-213(1996).
[3]
SEQUENCE FROM N.A. (ISOFORM MDM2-P90).
RC STRAIN=129/SV;
RX MEDLINE=96299630; PubMed=8660994;
RA de Oca Luna R.M., Tabor A.D., Eberspaecher H., Hulboy D.L.,
RA Worth L.L., Colman M.S., Finlay C.A., Lozano G.;
RT "The organization and expression of the mdm2 gene.";
RL Genomics 33:352-357(1996).
[4]
SEQUENCE FROM N.A. (ISOFORMS MDM2-P90 AND MDM2-P76).
RX MEDLINE=99175199; PubMed=10075719;
RA Saucedo L.J., Myers C.D., Perry M.E.;
RT "Multiple murine double minute gene 2 (MDM2) proteins are induced by
RT ultraviolet light.";
RL J. Biol. Chem. 274:8161-8168(1999).
[5]
NUCLEOLAR LOCALIZATION SIGNAL.
RX MEDLINE=20180080; PubMed=10713175;
RA Weber J.D., Kuo M.-L., Bothner B., DiGiannarino E.L., Kriwacki R.W.,
RA Roussel M.F., Sherr C.J.;
RT "Cooperative signals governing ARF-mdm2 interaction and nucleolar
RT localization of the complex.";
RL Mol. Cell. Biol. 20:2517-2528(2000).
[6]
PHOSPHORYLATION BY ATM.
RX MEDLINE=20079591; PubMed=10611322;

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RA "Rapid ATM-dependent phosphorylation of MDM2 precedes p53 accumulation
RT in response to DNA damage.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:14973-14977(1999).
CC -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and
CC apoptosis by binding its transcriptional activation domain.
CC Functions as a ubiquitin ligase E3, in the presence of E1 and E2,
CC toward p53 and itself. Permits the nuclear export of p53 and
CC targets it for proteasome-mediated proteolysis.
CC -!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity.
CC -!- SUBUNIT: Binds p53, p73, ARF(p14), ribosomal protein L5 and
CC specifically to RNA. Can interact also with retinoblastoma protein
CC (RB), E1A-associated protein EP300 and the E2F1 transcription
CC factor.
CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed
CC predominantly in the nucleoplasm. Interaction with ARF(p14)
CC results in the localization of both proteins to the nucleolus. The
CC nucleolar localization signals in both ARF(p14) and MDM2 may be
CC necessary to allow efficient nucleolar localization of both
CC proteins.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Mdm2-p90;
CC IsoId=P23804-1; Sequence=Displayed;
CC Note=Isoform Mdm2-p76 can also be produced by alternative
CC initiation at Met-50 of isoform Mdm2-p90, but is produced more
CC efficiently by alternative splicing;
CC Name=Mdm2-p76;
CC IsoId=P23804-2; Sequence=VSP_003215;
CC Note=Does not bind to p53;
CC Event=Alternative initiation;
CC Comment=2 isoforms, Mdm2-p90 (shown here) and Mdm2-p76, are
CC produced by alternative initiation at Met-1 and Met-50. Isoform
CC Mdm2-p76 is produced more efficiently by alternative splicing;
CC -!- TISSUE SPECIFICITY: Ubiquitously expressed at low-level throughout
CC embryo development and in adult tissues. MDM2-p90 is much more
CC abundant than MDM2-p76 in testis, brain, heart, and kidney, but in
CC the thymus, spleen, and intestine, the levels of the MDM2 proteins
CC are roughly equivalent.
CC -!- INDUCTION: By UV light.
CC -!- DOMAIN: Region 1 is sufficient for binding p53 and inhibiting its
CC G1 arrest and apoptosis functions. It also binds p73 and E2F1.
CC Region 11 contains most of a central acidic region required for
CC interaction with ribosomal protein L5 and a putative C4-type zinc
CC finger. The RING finger domain which coordinates two molecules of
CC zinc interacts specifically with RNA whether or not zinc is
CC present and mediates the hetero-oligomerization with MDM4. It is
CC also essential for its ubiquitin ligase E3 activity toward p53 and
CC itself.
CC -!- PTM: Phosphorylated in response to ionizing radiation in an ATM-
CC dependent manner.
CC -!- DISEASE: The gene for this protein is amplified in a mouse tumor
CC cell line.
CC -!- SIMILARITY: Belongs to the MDM2 / MDM4 family.
CC -!- SIMILARITY: Contains 1 RanBP2-type zinc finger.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC -!- SIMILARITY: Contains 1 SWIB domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X58876; CAA41684.1; -
CC EMBL; U40145; AAA91167.1; -
CC EMBL; U47944; AAB09030.1; -
CC EMBL; U47935; AAB09030.1; JOINED.
CC EMBL; U47936; AAB09030.1; JOINED.
CC EMBL; U47937; AAB09030.1; JOINED.
CC EMBL; U47938; AAB09030.1; JOINED.

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DR EMBL; U47939; AAB09030.1; JOINED.  
 DR EMBL; U47940; AAB09030.1; JOINED.  
 DR EMBL; U47941; AAB09030.1; JOINED.  
 DR EMBL; U47942; AAB09030.1; JOINED.  
 DR EMBL; U47943; AAB09030.1; JOINED.  
 DR EMBL; U47934; AAB09031.1; -.  
 DR PIR; S15349; S15349.  
 DR HGSP; Q9JMT8; 1YCR.  
 DR MGD; MGI.196952; Mdm2.  
 DR GO; GO:0005634; C:nucleus; IDA.  
 DR GO; GO:0005515; F:protein binding; IPI.  
 DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IDA.  
 DR GO; GO:0030163; P:protein catabolism; IDA.  
 DR GO; GO:0016567; P:protein ubiquitination; IDA.  
 DR GO; GO:0007089; P:traversing start control point of mitotic c. . .; IDA.  
 DR InterPro; IPR010984; MDM2.  
 DR InterPro; IPR003121; SWIB.  
 DR InterPro; IPR001876; Znf RangDP.  
 DR InterPro; IPR001841; Znf\_ring.  
 DR Pfam; PF02201; SWIB; 1.  
 DR Pfam; PF00641; Zf-RanBP; 1.  
 DR SMART; SM00184; RING; 1.  
 DR PROSITE; PS01358; ZF\_RANBP2\_1; 1.  
 DR PROSITE; PS01199; ZF\_RANBP2\_2; 1.  
 DR PROSITE; PS00518; ZF\_RING\_1; FALSE\_NEG.  
 DR PROSITE; PS50089; ZF\_RING\_2; 1.  
 DR Altermative initiation; Alternative splicing; Ligase; Metal-binding;  
 KW Nuclear protein; Phosphorylation; Proto-oncogene;  
 KW Ubiquitin-protein ligase E3 Mdm2, isoform  
 FT CHAIN 1 489 Ubiquitin-protein ligase E3 Mdm2, isoform  
 FT CHAIN 50 489 Ubiquitin-protein ligase E3 Mdm2, isoform  
 FT INIT MET 50 50 Mdm2-p76.  
 FT DOMAIN 27 107 For isoform Mdm2-p76.  
 FT DOMAIN 176 182 SWIB.  
 FT DOMAIN 183 195 Nuclear localization signal (Potential).  
 FT DOMAIN 203 213 Nuclear export signal.  
 FT DOMAIN 208 302 Poly-Ser.  
 FT DOMAIN 240 329 ARF-binding.  
 FT DOMAIN 221 299 Region II.  
 FT ZN\_FING 297 326 Asp/Glu-rich (acidic).  
 FT ZN\_FING 436 477 RanBP2-type.  
 FT ZN\_FING 464 471 RING-type.  
 FT VARSPLIC 1 49 Nucleolar localization signal (Potential).  
 FT CONFLICT 203 203 Missing (in isoform Mdm2-p76).  
 FT CONFLICT 419 419 /FTid=VSP\_003215.  
 FT CONFLICT 486 486 S -> T (in Ref. 1).  
 FT CONFLICT 489 AA; 54543 MW; 4ABF489E92038DF4 CRC64; D -> H (in Ref. 1).  
 FT SEQUENCE 489 AA; 54543 MW; 4ABF489E92038DF4 CRC64; S -> T (in Ref. 3).  
 Query Match 85.7%; Score 446.5; DB 1; Length 489;  
 Best Local Similarity 81.7%; Pred. No. 6.1e-43;  
 Matches 89; Conservative 7; Mismatches 10; Indels 3; Gaps 1;  
 QY 1 SQIPASEQTVRPKPLLLKLLKSGAOKDTVTMKELVXLYGQYIMTKRLYDEKQOHLVX 60  
 DB 17 SQIPASEQETLVRPKPLLLKLLKSGAQNDFYIMTKRLYDEKQOHLVY 76  
 QY 61 CSNDLXGLDGLFGVXSFVKEHRIYTWIXRNLNVNQQSSDSGTSVSEN 109  
 DB 77 CSNDLLGDVGVFSPFVKEHRIYTWIXRNLNVNQQSSDSGTSLSSES 122  
 RESULT 13  
 Q91XX7  
 ID Q91XX7 PRELIMINARY; PRT; 489 AA.  
 AC Q91XX7;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Mus musculus adult male lung cdna, RIKEN full-length enriched library,

DE DE clone:l200011P22 product:transformed mouse 3T3 cell double minute 2,  
 DE full insert sequence (transformed mouse 3T3 cell double minute 2) (Mus  
 DE musculus 2 days neonate thymus thymic cells cdna, RIKEN full-length  
 DE enriched library, clone:E43002B10 product:transformed mouse 3T3 cell  
 DE double minute 2, full insert sequence).  
 GN Name=Mdm2;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;  
 RX MEDLINE=99279253; PubMed=10349636;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [2]  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN [3]  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;  
 RA The FANTOM Consortium;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 RN [4]  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;  
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630(2000).  
 RN [5]  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;  
 RX MEDLINE=20530913; PubMed=11076861;  
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771(2000).  
 RN [6]  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Lung;  
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,  
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,  
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,  
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,  
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,  
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,  
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito K., Sakai C., Sakai K.,  
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,  
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,  
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
 RA Muramatsu M., Hayashizaki Y.;  
 RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Mouse;  
 RN RP

[illegible]



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OM protein - protein search, using sw model

Run on: January 27, 2005, 17:54:26 ; Search time 22.2 Seconds  
(without alignments)  
325.615 Million cell updates/sec

Title: US-10-822-254-4  
Perfect score: 521  
Sequence: 1 SQIPASEQETVVRPKPKLLK.....NLVVNQESSDSGTSVSEN 109

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	506	97.1	188	US-09-603-052-4	Sequence 4, Appli
2	506	97.1	491	US-07-903-103-2	Sequence 2, Appli
3	506	97.1	491	US-08-044-619A-2	Sequence 2, Appli
4	506	97.1	491	US-08-283-911-2	Sequence 2, Appli
5	506	97.1	491	US-08-245-500A-3	Sequence 3, Appli
6	506	97.1	491	US-08-390-546-3	Sequence 3, Appli
7	506	97.1	491	US-08-390-479A-3	Sequence 3, Appli
8	506	97.1	491	US-08-557-393-3	Sequence 3, Appli
9	506	97.1	491	US-08-390-516C-3	Sequence 3, Appli
10	506	97.1	491	US-08-390-517A-3	Sequence 3, Appli
11	506	97.1	491	US-08-390-515A-3	Sequence 3, Appli
12	506	97.1	491	US-08-801-718-3	Sequence 3, Appli
13	506	97.1	491	US-09-170-159A-3	Sequence 3, Appli
14	506	97.1	491	US-09-480-718-44	Sequence 44, Appli
15	489.5	94.0	216	US-09-510-252-4	Sequence 4, Appli
16	446.5	85.7	489	US-07-903-103-4	Sequence 4, Appli
17	446.5	85.7	489	US-08-044-619A-4	Sequence 4, Appli
18	446.5	85.7	489	US-08-283-911-4	Sequence 4, Appli
19	446.5	85.7	489	US-08-245-500A-5	Sequence 5, Appli
20	446.5	85.7	489	US-08-390-546-5	Sequence 5, Appli
21	446.5	85.7	489	US-08-390-479A-5	Sequence 5, Appli
22	446.5	85.7	489	US-08-557-393-5	Sequence 5, Appli
23	446.5	85.7	489	US-08-390-516C-5	Sequence 5, Appli
24	446.5	85.7	489	US-08-390-517A-5	Sequence 5, Appli
25	446.5	85.7	489	US-08-390-515A-5	Sequence 5, Appli
26	446.5	85.7	489	US-08-801-718-5	Sequence 5, Appli
27	446.5	85.7	489	US-09-170-159A-5	Sequence 5, Appli

28 446.5 85.7 489 4 US-09-480-718-46 Sequence 46, Appli  
29 166 31.9 243 4 US-03-786-702-2 Sequence 2, Appli  
30 68 13.1 206 3 US-09-311-311C-22 Sequence 22, Appli  
31 62.5 12.0 505 4 US-09-252-991A-29343 Sequence 29343, A  
32 62 11.9 1319 2 US-08-290-731C-2 Sequence 2, Appli  
33 62 11.9 1333 3 US-09-356-952-2 Sequence 2, Appli  
34 62 11.9 1333 4 US-09-976-594-312 Sequence 312, App  
35 62 11.9 1336 2 US-08-290-731C-6 Sequence 6, Appli  
36 61.5 11.8 658 4 US-09-248-796A-17674 Sequence 17674, A  
37 61 11.7 242 4 US-09-489-039A-8331 Sequence 8331, Ap  
38 61 11.7 482 4 US-09-248-796A-17755 Sequence 17755, A  
39 59.5 11.4 194 3 US-09-117-257-17 Sequence 17, Appl  
40 59.5 11.4 194 3 US-08-945-476-17 Sequence 17, Appl  
41 59.5 11.4 194 3 US-09-489-352-17 Sequence 17, Appl  
42 59.5 11.4 712 4 US-09-248-796A-19645 Sequence 19645, A  
43 59 11.3 781 4 US-09-486-147-3 Sequence 3, Appli  
44 58.5 11.2 145 4 US-09-270-767-43660 Sequence 43660, A  
45 58 11.1 793 4 US-09-107-532A-6223 Sequence 6223, Ap

#### ALIGNMENTS

##### RESULT 1

US-09-603-052-4  
; Sequence 4, Application US/09603052  
; Patent No. 6492116  
; GENERAL INFORMATION:  
; APPLICANT: Chene, Patrick  
; APPLICANT: Hochkeppel, Heinz-Kurt  
; TITLE OF INVENTION: Assay for identifying inhibitors of the interaction  
; TITLE OF INVENTION: between proteins p53 and dm2  
; FILE REFERENCE: MEMB26.001C1  
; CURRENT APPLICATION NUMBER: US/09/603,052  
; CURRENT FILING DATE: 2000-06-26  
; PRIOR APPLICATION NUMBER: EP 95810576.9  
; PRIOR FILING DATE: 1995-09-18  
; PRIOR APPLICATION NUMBER: PCT/EP96/03957  
; PRIOR FILING DATE: 1996-09-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 188  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-603-052-4

Query Match 97.1%; Score 506; DB 4; Length 188;  
Best Local Similarity 93.6%; Pred. No. 2.9e-60;  
Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 SQIPASEQETVVRPKPKLLKLLKSVGAQKDTYTMKEVLXLYLGQYIMTKRLYDEKQOHVX 60

Db 17 SQIPASEQETLVVRPKPAPLLKLLKSVGAQKDTYTMKEVLFLYLGQYIMTKRLYDEKQOHVY 76

Qy 61 CSNDLXGDLFGVGSFVSKEHKKIYTMIXRNLVVVNQQSSDSGTSVSEN 109

Db 77 CSNDLXGDLFGVGSFVSKEHKKIYTMIXRNLVVVNQQSSDSGTSVSEN 125

##### RESULT 2

US-07-903-103-2  
; Sequence 2, Application US/07903103  
; Patent No. 5411860  
; GENERAL INFORMATION:  
; APPLICANT: VOGELSTEIN, BERT  
; APPLICANT: KINZLER, KENNETH  
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
; TITLE OF INVENTION: HUMAN TUMORS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
; STREET: 1001 G ST., N.W.

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; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/903,103
; FILING DATE: 19920623
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/867,840
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.40148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-903-103-2

Query Match 97.1%; Score 506; DB 1; Length 491;
Best Local Similarity 93.6%; Pred. No. 1e-59;
Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 SQIPASEQETXVRPKPLLLKLLKSVGAQDVTYTMKEVLXVYLGQYIMTKRLYDEKQOHIVX 60
DB 17 SQIPASEQETLVRPKPLLLKLLKSVGAQDVTYTMKEVLVFLYLGQYIMTKRLYDEKQOHIVY 76
QY 61 CSNDXLGDLFGVXSFVSKHRKIYTWIYRNLVVNNQESSDSGTSVSEN 109
DB 77 CSNDLLGDLFGVPSFVSKHRKIYTWIYRNLVVNNQESSDSGTSVSEN 125

; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
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; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/044,619A
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/903,103
; FILING DATE: 23-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.40148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-044-619A-2

Query Match 97.1%; Score 506; DB 1; Length 491;
Best Local Similarity 93.6%; Pred. No. 1e-59;
Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 SQIPASEQETXVRPKPLLLKLLKSVGAQDVTYTMKEVLXVYLGQYIMTKRLYDEKQOHIVX 60
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QY 61 CSNDXLGDLFGVXSFVSKHRKIYTWIYRNLVVNNQESSDSGTSVSEN 109
DB 77 CSNDLLGDLFGVPSFVSKHRKIYTWIYRNLVVNNQESSDSGTSVSEN 125

; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/044,619A
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/903,103
; FILING DATE: 23-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.40148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-044-619A-2

Query Match 97.1%; Score 506; DB 1; Length 491;
Best Local Similarity 93.6%; Pred. No. 1e-59;
Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 SQIPASEQETXVRPKPLLLKLLKSVGAQDVTYTMKEVLXVYLGQYIMTKRLYDEKQOHIVX 60
DB 17 SQIPASEQETLVRPKPLLLKLLKSVGAQDVTYTMKEVLVFLYLGQYIMTKRLYDEKQOHIVY 76
QY 61 CSNDXLGDLFGVXSFVSKHRKIYTWIYRNLVVNNQESSDSGTSVSEN 109
DB 77 CSNDLLGDLFGVPSFVSKHRKIYTWIYRNLVVNNQESSDSGTSVSEN 125

; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/283,911
; FILING DATE: 07-APR-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/903,103
; FILING DATE: 23-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.40148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-283-911-2

Query Match 97.1%; Score 506; DB 1; Length 491;
Best Local Similarity 93.6%; Pred. No. 1e-59;
Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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QY 61 CSNDXLGDLFGVXSFVSKHRKIYTWIYRNLVVNNQESSDSGTSVSEN 109
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; CITY: WASHINGTON
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; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; FILING DATE: 07-APR-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/903,103
; FILING DATE: 23-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.40148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
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; MOLECULE TYPE: protein
; US-08-283-911-2

Query Match 97.1%; Score 506; DB 1; Length 491;
Best Local Similarity 93.6%; Pred. No. 1e-59;
Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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QY 61 CSNDXLGDLFGVXSFVSKHRKIYTWIYRNLVVNNQESSDSGTSVSEN 109
DB 77 CSNDLLGDLFGVPSFVSKHRKIYTWIYRNLVVNNQESSDSGTSVSEN 125

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; FILING DATE: 07-APR-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/903,103
; FILING DATE: 23-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.40148
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; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-283-911-2

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DB 77 CSNDLLGDLFGVPSFVSKHRKIYTWIYRNLVVNNQESSDSGTSVSEN 125

; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/283,911
; FILING DATE: 07-APR-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/903,103
; FILING DATE: 23-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.40148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-283-911-2

Query Match 97.1%; Score 506; DB 1; Length 491;
Best Local Similarity 93.6%; Pred. No. 1e-59;
Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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DB 17 SQIPASEQETLVRPKPLLLKLLKSVGAQDVTYTMKEVLVFLYLGQYIMTKRLYDEKQOHIVY 76
QY 61 CSNDXLGDLFGVXSFVSKHRKIYTWIYRNLVVNNQESSDSGTSVSEN 109
DB 77 CSNDLLGDLFGVPSFVSKHRKIYTWIYRNLVVNNQESSDSGTSVSEN 125

; CITY
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DB 77 CSNDLLGDLFGVPSFSVKEHKIKYTIYRNLVVVNQESSDSGTSVSEN 125

RESULT 6  
US-08-390-546-3  
; Sequence 3, Application US/08390546  
; Patent No. 5606044  
; GENERAL INFORMATION:  
; APPLICANT: BURRELL, MARILEE  
; APPLICANT: HILL, DAVID E.  
; APPLICANT: KINZLER, KENNETH W.  
; APPLICANT: VOGELSTEIN, BERT  
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
; TITLE OF INVENTION: HUMAN TUMORS  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
; STREET: 1001 G STREET, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/390,546  
; FILING DATE: 07-APR-1993  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KAGAN, SARAH A.  
; REGISTRATION NUMBER: 32,141  
; REFERENCE/DOCKET NUMBER: 01107.42798  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-508-9100  
; TELEFAX: 202-508-9299  
; TELEX: 197430 BMB UT  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 491 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-390-546-3

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Best Local Similarity 93.8%; Pred. No. 1e-59; Indels 0; Gaps 0;  
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DB 17 SQIPASEQETLVRPKPKLLKLLKSVGAQKDTYTMKEVLFLVGQYIMTKRLYDEKQOHVY 76

QY 61 CSNDXLDGLDFGVXSFVSKYHKIKYTIYRNLVVVNQESSDSGTSVSEN 109  
DB 77 CSNDLLGDLFGVPSFSVKEHKIKYTIYRNLVVVNQESSDSGTSVSEN 125

RESULT 7  
US-08-390-479A-3  
; Sequence 3, Application US/08390479A  
; Patent No. 5618921  
; GENERAL INFORMATION:  
; APPLICANT: BURRELL, MARILEE  
; APPLICANT: HILL, DAVID E.  
; APPLICANT: KINZLER, KENNETH W.  
; APPLICANT: VOGELSTEIN, BERT  
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
; TITLE OF INVENTION: HUMAN TUMORS  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:

```
; ADDRESSEE: BANNER & WITCOFF, LTD.
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,479A
; FILING DATE: 02-FEB-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.48992
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 3:
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-390-479A-3

Query Match 97.1%; Score 506; DB 1; Length 491;
Best Local Similarity 93.6%; Pred. No. 1e-59;
Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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DB 17 SQIPASEQETLVRPKPLLLKLLKLSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76
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RESULT 8
US-08-557-393-3
; Sequence 3, Application US/08557393
; Patent No. 5702903
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,393
; FILING DATE: 13-NOV-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

; ADDRESSEE: BANNER & WITCOFF, LTD.
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; APPLICATION NUMBER: US/08/557,393
; FILING DATE: 13-NOV-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/245,500
; FILING DATE: 18-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-557-393-3

Query Match 97.1%; Score 506; DB 1; Length 491;
Best Local Similarity 93.6%; Pred. No. 1e-59;
Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 SQIPASEQETXVRPKPXLKLLKLSVGAQKDTYTMKEVLXLYGQYIMTKRLYDEKQOHIVX 60
DB 17 SQIPASEQETLVRPKPLLLKLLKLSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76
QY 61 CSNDXLGDLFGVKSFSVKEHRKIYTMIXRNLVVNQESSDSGTSVSEN 109
DB 77 CSNDLLGDLFGVPSFVKEHRKIYTMIRNLVVNQESSDSGTSVSEN 125

RESULT 9
US-08-390-516C-3
; Sequence 3, Application US/08390516C
; Patent No. 5708136
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,516C
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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US-08-390-516C-3

Query Match 97.1%; Score 506; DB 1; Length 491;  
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 Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 SQIPASEQETVVRPKPXLKLLKSVGAQKDTYTKMKEVLXYLGQYIMTKRLYDEKQOHIYV 60  
 Db 17 SQIPASEQETLVVRPKPXLKLLKSVGAQKDTYTKMKEVLXYLGQYIMTKRLYDEKQOHIYV 76

Qy 61 CSNDXLGDLFGVXSFVSKHRKIYTMIXRNLVNVNQESSDGSVSEN 109  
 Db 77 CSNDLLGDLFGVPSFVSKHRKIYTMIXRNLVNVNQESSDGSVSEN 125

RESULT 10

US-08-390-517A-3  
 ; Sequence 3, Application US/08390517A  
 ; Patent No. 5736338  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BURRELL, MARILEE  
 ; APPLICANT: HILL, DAVID E.  
 ; APPLICANT: KINZLER, KENNETH W.  
 ; APPLICANT: VOGELSTEIN, BERT  
 ; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
 ; TITLE OF INVENTION: HUMAN TUMORS  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
 ; STREET: 1001 G STREET, N.W.  
 ; CITY: WASHINGTON  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20001  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/390,517A  
 ; FILING DATE: 07-APR-1993  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: KAGAN, SARAH A.  
 ; REGISTRATION NUMBER: 32,141  
 ; REFERENCE/DOCKET NUMBER: 01107.42798  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-508-9100  
 ; TELEFAX: 202-508-9299  
 ; TELEX: 197430 BBMB UT  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 491 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 US-08-390-517A-3

Query Match 97.1%; Score 506; DB 1; Length 491;  
 Best Local Similarity 93.6%; Pred. No. 1e-59;  
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Qy 1 SQIPASEQETVVRPKPXLKLLKSVGAQKDTYTKMKEVLXYLGQYIMTKRLYDEKQOHIYV 60  
 Db 17 SQIPASEQETLVVRPKPXLKLLKSVGAQKDTYTKMKEVLXYLGQYIMTKRLYDEKQOHIYV 76

Qy 61 CSNDXLGDLFGVXSFVSKHRKIYTMIXRNLVNVNQESSDGSVSEN 109  
 Db 77 CSNDLLGDLFGVPSFVSKHRKIYTMIXRNLVNVNQESSDGSVSEN 125

RESULT 11

US-08-390-515A-3

; Sequence 3, Application US/08390515A  
 ; Patent No. 5756455  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BURRELL, MARILEE  
 ; APPLICANT: HILL, DAVID E.  
 ; APPLICANT: KINZLER, KENNETH W.  
 ; APPLICANT: VOGELSTEIN, BERT  
 ; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
 ; TITLE OF INVENTION: HUMAN TUMORS  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
 ; STREET: 1001 G STREET, N.W.  
 ; CITY: WASHINGTON  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20001  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/390,515A  
 ; FILING DATE: 07-APR-1993  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: KAGAN, SARAH A.  
 ; REGISTRATION NUMBER: 32,141  
 ; REFERENCE/DOCKET NUMBER: 01107.42798  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-508-9100  
 ; TELEFAX: 202-508-9299  
 ; TELEX: 197430 BBMB UT  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 491 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 US-08-390-515A-3

Query Match

Best Local Similarity 97.1%; Score 506; DB 1; Length 491;  
 Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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 Db 17 SQIPASEQETLVVRPKPXLKLLKSVGAQKDTYTKMKEVLXYLGQYIMTKRLYDEKQOHIYV 76

Qy 61 CSNDXLGDLFGVXSFVSKHRKIYTMIXRNLVNVNQESSDGSVSEN 109  
 Db 77 CSNDLLGDLFGVPSFVSKHRKIYTMIXRNLVNVNQESSDGSVSEN 125

RESULT 12

US-08-801-718-3  
 ; Sequence 3, Application US/08801718  
 ; Patent No. 5858976  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BURRELL, MARILEE  
 ; APPLICANT: HILL, DAVID E.  
 ; APPLICANT: KINZLER, KENNETH W.  
 ; APPLICANT: VOGELSTEIN, BERT  
 ; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
 ; TITLE OF INVENTION: HUMAN TUMORS  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
 ; STREET: 1001 G STREET, N.W.  
 ; CITY: WASHINGTON  
 ; STATE: D.C.

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; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,718
; FILING DATE: 14-FEB-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/390,515
; FILING DATE: 07-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-801-718-3

Query Match          97.1%; Score 506; DB 2; Length 491;
Best Local Similarity 93.6%; Pred. No. 1e-59;
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QY 61 CSNDXLGDLFGVXSFVSKEHRKIYTMIXRNLVNVNQESSDSGTSVSEN 109
DB 77 CSNDLLGDLFGVPSFVSKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 125

RESULT 13
US-09-170-159A-3
; Sequence 3, Application US/09170159A
; Patent No. 6399755
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; HILL, DAVID E.
; KINZLER, KENNETH W.
; VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/170,159A
; FILING DATE: 13-Oct-1998
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.

; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,718
; FILING DATE: 14-FEB-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/390,515
; FILING DATE: 07-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-801-718-3

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Best Local Similarity 93.6%; Pred. No. 1e-59;
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DB 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDXLGDLFGVXSFVSKEHRKIYTMIXRNLVNVNQESSDSGTSVSEN 109
DB 77 CSNDLLGDLFGVPSFVSKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 125

RESULT 14
US-09-480-718-44
; Sequence 44, Application US/09480718
; Patent No. 6407062
; GENERAL INFORMATION:
; APPLICANT: Sherr, Charles J
; APPLICANT: Quelle, Dawn E
; APPLICANT: Weber, Jason D.
; APPLICANT: Rousssel, Martine F.
; APPLICANT: Frederique, Zindy
; TITLE OF INVENTION: ARF-19, A NOVEL REGULATOR OF THE MAMMALIAN CELL CYCLE
; FILE REFERENCE: 1340-1-023 CIP 1
; CURRENT APPLICATION NUMBER: US/09/480,718
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 09/129,855
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 44
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-480-718-44

Query Match          97.1%; Score 506; DB 4; Length 491;
Best Local Similarity 93.6%; Pred. No. 1e-59;
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DB 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDXLGDLFGVXSFVSKEHRKIYTMIXRNLVNVNQESSDSGTSVSEN 109
DB 77 CSNDLLGDLFGVPSFVSKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 125

RESULT 15
US-09-510-252-4
; Sequence 4, Application US/09510252
; Patent No. 6372490
; GENERAL INFORMATION:
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Yang, Meijia
; APPLICANT: Schulz, Vincent

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; APPLICANT: CuraGen Corporation
; TITLE OF INVENTION: MDM INTERACTING PROTEIN AND METHODS OF USE THEREOF
; FILE REFERENCE: 15966-524 MDM US
; CURRENT APPLICATION NUMBER: US/09/510,252
; CURRENT FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: USSN 60/121,192
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: USSN 60/122,643
; PRIOR FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 4
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; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-510-252-4

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Copyright (c) 1993 - 2005 CompuGen Ltd.

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	506	97.1	491	US-09-956-425-8	Sequence 8, Appli
3	506	97.1	491	US-09-029-327-2	Sequence 2, Appli
4	506	97.1	491	US-09-966-724-2	Sequence 2, Appli
5	506	97.1	491	US-10-422-536-137	Sequence 137, App
6	506	97.1	491	US-10-232-351-35	Sequence 35, Appl
7	506	97.1	491	US-10-685-838-1	Sequence 1, Appli
8	506	97.1	491	US-10-724-225-2	Sequence 2, Appli
9	506	97.1	491	US-10-489-802-8	Sequence 8, Appli
10	506	97.1	491	US-10-723-860-2236	Sequence 236, Ap
11	489.5	94.0	216	US-10-057-510-4	Sequence 4, Appli
12	480.5	92.2	522	US-10-287-226-380	Sequence 380, App
13	480.5	92.2	522	US-10-287-226-382	Sequence 382, App

14	446.5	85.7	489	9	US-09-956-425-6	Sequence 6, Appli
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16	446.5	85.7	489	17	US-10-489-802-6	Sequence 6, Appli
17	439	84.3	95	17	US-10-685-838-2	Sequence 2, Appli
18	430	82.5	95	17	US-10-685-838-4	Sequence 4, Appli
19	426	81.8	92	17	US-10-685-838-3	Sequence 3, Appli
20	285	54.7	59	14	US-10-211-088-143	Sequence 143, App
21	71	13.6	472	14	US-10-369-493-16585	Sequence 16585, A
22	71	13.6	473	15	US-10-282-122A-45311	Sequence 45311, A
23	70.5	13.5	328	17	US-10-425-115-191466	Sequence 191466, A
24	69.5	13.3	291	15	US-10-425-114-59572	Sequence 59572, A
25	69.5	13.3	291	17	US-10-425-115-191465	Sequence 191465, A
26	68	13.1	683	14	US-10-369-493-2188	Sequence 2188, Ap
27	65.5	12.6	332	15	US-10-425-114-47234	Sequence 47234, A
28	65.5	12.6	332	16	US-10-437-963-174237	Sequence 174237, A
29	65	12.5	312	15	US-10-282-122A-46159	Sequence 46159, A
30	65	12.5	757	16	US-10-437-963-156834	Sequence 156834, A
31	64.5	12.4	467	14	US-10-362-774-3	Sequence 3, Appli
32	64.5	12.4	467	14	US-10-369-493-6071	Sequence 6071, Ap
33	64	12.3	413	14	US-10-369-493-17318	Sequence 17318, A
34	64	12.3	1448	16	US-10-437-963-138597	Sequence 138597, A
35	63.5	12.2	226	17	US-10-494-087-18	Sequence 18, Appl
36	63.5	12.2	425	16	US-10-420-083-6	Sequence 6, Appli
37	63.5	12.2	505	15	US-10-437-963-161869	Sequence 161869, A
38	63.5	12.2	709	15	US-10-282-122A-63455	Sequence 63455, A
39	63.5	12.2	821	16	US-10-437-963-110602	Sequence 110602, A
40	63	12.1	1031	16	US-10-437-963-189155	Sequence 189155, A
41	62.5	12.0	226	14	US-10-091-007-210	Sequence 210, App
42	62.5	12.0	451	14	US-10-369-493-17149	Sequence 17149, A
43	62.5	12.0	486	15	US-10-425-114-43529	Sequence 43529, A
44	62.5	12.0	2932	16	US-10-437-963-120244	Sequence 120244, A
45	62	11.9	128	17	US-10-425-115-232489	Sequence 232489, A

## ALIGNMENTS

RESULT 1  
US-09-888-077-1  
; Sequence 1, Application US/09888077  
; Patent No. US2002003181A1  
; GENERAL INFORMATION:  
; APPLICANT: Ronai, Ze'ev  
; TITLE OF INVENTION: Modification of Mdm2 Activity  
; FILE REFERENCE: 2420/1H195-US1  
; CURRENT APPLICATION NUMBER: US/09/888,077  
; CURRENT FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: US 60/213,343  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 491  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-888-077-1

Query Match	97.1%	Score	506;	DB	9;	Length	491;
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; Sequence 8, Application US/09956425
; Patent No. US20020045192A1
; GENERAL INFORMATION:
; APPLICANT: Kriwacki, Richard
; APPLICANT: Bothner, Brian
; APPLICANT: Lewis, William
; TITLE OF INVENTION: Aif and Hdm2 Interaction Domains and Method of Use Thereof
; FILE REFERENCE: 1340/1/035
; CURRENT APPLICATION NUMBER: US/09/956,425
; CURRENT FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-956-425-8

Query Match          97.1%; Score 506; DB 9; Length 491;
Best Local Similarity 93.6%; Pred. No. 2e-55;
Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVPRPKPLLLKLLKSVGAQKDTYTMKEVLXLYLGQYIMTKRLYDEKQOHIVX 60
DB 17 SQIPASEQETLVPRPKPLLLKLLKSVGAQKDTYTMKEVLXLYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDXLGDLFGVXSFVSKHRKIYTMIXRNLLVNVNQESSDSGTSVSEN 109
DB 77 CSNDLLGDLFGVPSFVSKHRKIYTMIXRNLLVNVNQESSDSGTSVSEN 125

RESULT 3
US-09-029-327-2
; Sequence 2, Application US/09029327
; Publication No. US20030060432A1
; GENERAL INFORMATION:
; APPLICANT: TOCQUE, Bruno
; APPLICANT: WASLYK, Bohdan
; APPLICANT: DUBS-POTERSZMAN,
; APPLICANT: Marie-Christine
; TITLE OF INVENTION: ANTAGONISTS OF THE ONCOGENIC ACTIVITY OF
; TITLE OF INVENTION: THE PROTEIN MDM2, AND USE THEREOF IN THE TREATMENT OF
; TITLE OF INVENTION: CANCERS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.,
; STREET: 500 Arcola Road, Mailstop 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/029,327
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 96/01340
; FILING DATE: 02-SEP-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO FR95/10331
; FILING DATE: 04-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Rehlner Esq., Paul F.
; REGISTRATION NUMBER: 35,135
; REFERENCE/DOCKET NUMBER: ST95050-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808

```

```

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-029-327-2

Query Match          97.1%; Score 506; DB 10; Length 491;
Best Local Similarity 93.6%; Pred. No. 2e-55;
Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVPRPKPLLLKLLKSVGAQKDTYTMKEVLXLYLGQYIMTKRLYDEKQOHIVX 60
DB 17 SQIPASEQETLVPRPKPLLLKLLKSVGAQKDTYTMKEVLXLYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDXLGDLFGVXSFVSKHRKIYTMIXRNLLVNVNQESSDSGTSVSEN 109
DB 77 CSNDLLGDLFGVPSFVSKHRKIYTMIXRNLLVNVNQESSDSGTSVSEN 125

RESULT 4
US-09-966-724-2
; Sequence 2, Application US/09966724
; Publication No. US20040170971A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G ST., N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/966,724
; FILING DATE: 01-Oct-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/044,619
; FILING DATE: 2001-10-01
; APPLICATION NUMBER: US 07/867,840
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.40148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BMB UT
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
; US-09-966-724-2

Query Match          97.1%; Score 506; DB 11; Length 491;
Best Local Similarity 93.6%; Pred. No. 2e-55;
Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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; OTHER INFORMATION: (mdm2) homolog full length protein isoform, mouse  
 ; OTHER INFORMATION: p53-binding protein (MDM2) homolog, transcript  
 ; OTHER INFORMATION: variant MDM2, transformed 3T3 cell double minute 2  
 ; OTHER INFORMATION: Mdm2 cDNA  
 US-110-232-951-35

	Query Match	97.1%	Score 506;	DB 15;	Length 491;
	Best Local Similarity	93.6%;	Pred. No. 2e-55;		
	Matches 102;	Conservative 0;	Mismatches 7;	Indels 0;	Gaps 0;
Qy	1	SQIPASEQETXVRPKPXLKLLKLSVGAQKDTYTMKEVLYLGQYIMTKRLYDESKQHIVX	60		
Db	17	SQIPASEQETLVRPKPLLLKLLSVGAQKDTYTMKEVLYLGQYIMTKRLYDESKQHIVY	76		
Qy	61	CSNDXLDGLPGVXSFSVKHEHRTYIMYXRLVNVNQESDSDGTSVSEN	109		
Db	77	CSNDLGLDIPGVPSFSVKHEHRTYIMYXRLVNVNQESDSDGTSVSEN	125		

	Query Match	97.1%	Score 506;	DB 17;	Length 491;
	Best Local Similarity	93.8%;	Pred. No. 2e-55;	Indels 0;	Gaps 0;
	Matches 102;	Conservative	0;	Mismatches	7;
QY	1	SQIPASEQETXVRPKLLKLKLSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQOHIVX	60		
Db	17	SQIPASEQETLVRPKLLKLKLSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQOHIVY	76		
QY	61	CSNDXLGDLFGVXSFVKSEHRRKIYTIMRNLVVNQOESSDSTGTSYSEN	109		
Db	77	CSNDLGLDIFGVPSFVKSEHRRKIYTIMRNLVVNQOESSDSTGTSYSEN	125		

RESULT 8  
US-10-724-225-2  
; Sequence 2, Application US/10724225  
; Publication No. US20040209834A1  
; GENERAL INFORMATION:  
; APPLICANT: TOCOUE, Bruno  
; WASYLYK, Bohdan  
; DUBS-POTERSZMAN,  
; Marie-Christine  
; TITLE OF INVENTION: ANTAGONISTS OF THE ONCOGENIC ACTIVITY OF  
; THE PROTEIN MDM2, AND USE THEREOF IN THE  
; CANCERS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rhone-Poulenc Rorer Inc.  
; STREET: 500 Arcola Road, Mailstop 3C43  
; CITY: Collegeville

STATE: PA  
COUNTRY: USA  
ZIP: 19426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/724,225  
FILING DATE: 01-Dec-2003  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/029,327  
FILING DATE: <unknown>  
APPLICATION NUMBER: FR 96/01340  
FILING DATE: 02-SEP-1996  
APPLICATION NUMBER: WO FR95/10331  
FILING DATE: 04-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Fehner Esq., Paul F.  
REGISTRATION NUMBER: 35,135  
REFERENCE/DOCKET NUMBER: ST95050-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 454-3839  
TELEFAX: (610) 454-3808  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 491 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-724-225-2

Query Match 97.1%; Score 506; DB 17; Length 491;  
Best Local Similarity 93.6%; Pred. No. 2e-55;  
Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
QY 1 SQIPASEQETVVRPKPXLKLLKSVGAQKDTYTMKEVLXVLGYIMTKRLYDEKQOHIVX 60  
DB 17 SQIPASEQETVVRPKPXLKLLKSVGAQKDTYTMKEVLXVLGYIMTKRLYDEKQOHIVY 76  
QY 61 CSNDXLGDLFGVXSFVSKHRKIYTMIXRNLVVNVNQESSDSTSVSEN 109  
DB 77 CSNDLLGDLFGVPSFVSKHRKIYTMIXRNLVVNVNQESSDSTSVSEN 125

RESULT 9  
US-10-489-802-8  
Sequence 8, Application US/10489802  
Publication No. US20040248198A1  
GENERAL INFORMATION:  
APPLICANT: St. Jude Children's Research Hospital, Inc.  
APPLICANT: Kriwacki, Richard  
APPLICANT: Bothner, Brian  
APPLICANT: Lewis, William  
TITLE OF INVENTION: Aif and Hdm2 Interaction Domains and  
TITLE OF INVENTION: Method of Use Thereof  
FILE REFERENCE: 44158/243642  
CURRENT APPLICATION NUMBER: US/10/489,802  
CURRENT FILING DATE: 2004-03-16  
PRIOR APPLICATION NUMBER: US 09/956,425  
PRIOR FILING DATE: 2001-09-19  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 491  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-489-802-8

Query Match 97.1%; Score 506; DB 17; Length 491;

Best Local Similarity 93.6%; Pred. No. 2e-55;  
Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
QY 1 SQIPASEQETVVRPKPXLKLLKSVGAQKDTYTMKEVLXVLGYIMTKRLYDEKQOHIVX 60  
DB 17 SQIPASEQETVVRPKPXLKLLKSVGAQKDTYTMKEVLXVLGYIMTKRLYDEKQOHIVY 76  
QY 61 CSNDXLGDLFGVXSFVSKHRKIYTMIXRNLVVNVNQESSDSTSVSEN 109  
DB 77 CSNDLLGDLFGVPSFVSKHRKIYTMIXRNLVVNVNQESSDSTSVSEN 125

RESULT 10  
US-10-723-860-2236  
Sequence 2236, Application US/10723860  
Publication No. US20040253606A1  
GENERAL INFORMATION:  
APPLICANT: Aziz, Natasha  
APPLICANT: Ginsburg, Wendy M.  
APPLICANT: Zlotnik, Albert  
TITLE OF INVENTION: Methods for Diagnosis of Soft Tissue Sarcoma, Compositions &  
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators  
FILE REFERENCE: 05882.0193.NPUS01  
CURRENT APPLICATION NUMBER: US/10/723,860  
CURRENT FILING DATE: 2003-11-26  
PRIOR APPLICATION NUMBER: 60/429,739  
PRIOR FILING DATE: 2002-11-26  
NUMBER OF SEQ ID NOS: 8393  
SOFTWARE: Patent in version 3.2  
SEQ ID NO 2236  
LENGTH: 491  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-723-860-2236

Query Match 97.1%; Score 506; DB 17; Length 491;  
Best Local Similarity 93.6%; Pred. No. 2e-55;  
Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
QY 1 SQIPASEQETVVRPKPXLKLLKSVGAQKDTYTMKEVLXVLGYIMTKRLYDEKQOHIVX 60  
DB 17 SQIPASEQETVVRPKPXLKLLKSVGAQKDTYTMKEVLXVLGYIMTKRLYDEKQOHIVY 76  
QY 61 CSNDXLGDLFGVXSFVSKHRKIYTMIXRNLVVNVNQESSDSTSVSEN 109  
DB 77 CSNDLLGDLFGVPSFVSKHRKIYTMIXRNLVVNVNQESSDSTSVSEN 125

RESULT 11  
US-10-057-510-4  
Sequence 4, Application US/10057510  
Publication No. US20020098580A1  
GENERAL INFORMATION:  
APPLICANT: Nandabalan, Krishnan  
APPLICANT: Yang, Meljia  
APPLICANT: Schulz, Vincent  
APPLICANT: Curagen Corporation  
TITLE OF INVENTION: MDM INTERACTING PROTEIN AND METHODS OF USE THEREOF  
FILE REFERENCE: 15966-524 MDM US  
CURRENT APPLICATION NUMBER: US/10/057,510  
CURRENT FILING DATE: 2002-01-25  
PRIOR APPLICATION NUMBER: USSN 09/510,252  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: USSN 60/121,192  
PRIOR FILING DATE: 1999-02-23  
PRIOR APPLICATION NUMBER: USSN 60/122,643  
PRIOR FILING DATE: 1999-03-03  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 4  
LENGTH: 216  
TYPE: PRT  
ORGANISM: Homo sapiens





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; APPLICANT: Vernet, Corine A.M.,
; APPLICANT: Zerhusen, Bryan D.,
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-480C
; CURRENT APPLICATION NUMBER: US/10/287,226
; CURRENT FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: 60/334,421
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/354,392
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/360,148
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: 60/364,000
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/404,821
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 60/334,526
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/354,409
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/364,227
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/334,027
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/331,641
; PRIOR FILING DATE: 2001-11-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 673
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 382
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-226-382

Query Match      92.2%; Score 480.5; DB 15; Length 522;
Best Local Similarity 72.9%; Pred. No. 3.7e-52;
Matches 102; Conservative 0; Mismatches 7; Indels 31; Gaps 1;

Qy      1  SQIPASEQETXVRPKPXLKLLKSVGAQKDTYTMKE----- 36
Db      17  SQIPASEQETTLVRPKPLLLKLLKSVGAQKDTYTMKERWSFTMLPRLVWNSWAQICLPRP 76
Qy      37  -----VLXVLGQVIMTKRLYDEKQHHVXCSNDXLDGLFCGVXSVKHEHRKIYTMIXR 89
Db      77  PKVLDLQVLFYLGQVIMTKRLYDEKQHHVYCSNDLLGLDFGVPSFKHEHRKIYTMIR 136

Qy      90  NLVVVNQOESSDSGTSVSEN 109
Db      137  NLVVVNQOESSDSGTSVSEN 156

RESULT 14
US-09-956-425-6
; Sequence 6, Application US/09956425
; Patent No. US20020045192A1
; GENERAL INFORMATION:
; APPLICANT: Kriwacki, Richard
; APPLICANT: Bothner, Brian
; APPLICANT: Lewis, William
; TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and Method of Use Thereof
; CURRENT APPLICATION NUMBER: US/09/956,425
; CURRENT FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-956-425-6

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Query Match      85.7%; Score 446.5; DB 9; Length 489;
Best Local Similarity 81.7%; Pred. No. 7.3e-48;
Matches 89; Conservative 7; Mismatches 10; Indels 3; Gaps 1;

Qy      1  SQIPASEQETXVRPKPXLKLLKSVGAQKDTYTMKEVLXVLGQVIMTKRLYDEKQHHVX 60
Db      17  SQIPASEQETTLVRPKPLLLKLLKSVGAQNDTYTMKEIIFYIGQVIMTKRLYDEKQHHVY 76
Qy      61  CSNDXLDGLFCGVXSVKHEHRKIYTMIXRNLVVVNQOESSDSGTSVSEN 109
Db      77  CSNDLLGDVFGVPSFKHEHRKIYAMIRNLVAVSQ---DSGTSLSSES 122

RESULT 15
US-09-966-724-4
; Sequence 4, Application US/09966724
; Publication No. US20040170971A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G ST., N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/966,724
; FILING DATE: 01-Oct-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/044,619
; FILING DATE: 2001-10-01
; APPLICATION NUMBER: US 07/867,840
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.40148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-966-724-4

Query Match      85.7%; Score 446.5; DB 11; Length 489;
Best Local Similarity 81.7%; Pred. No. 7.3e-48;
Matches 89; Conservative 7; Mismatches 10; Indels 3; Gaps 1;

Qy      1  SQIPASEQETXVRPKPXLKLLKSVGAQKDTYTMKEVLXVLGQVIMTKRLYDEKQHHVX 60
Db      17  SQIPASEQETTLVRPKPLLLKLLKSVGAQNDTYTMKEIIFYIGQVIMTKRLYDEKQHHVY 76
Qy      61  CSNDXLDGLFCGVXSVKHEHRKIYTMIXRNLVVVNQOESSDSGTSVSEN 109
Db      77  CSNDLLGDVFGVPSFKHEHRKIYAMIRNLVAVSQ---DSGTSLSSES 122

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Search completed: January 27, 2005, 18:23:04  
Job time : 69.4 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 27, 2005, 17:45:30 ; Search time 80.8 Seconds  
(without alignments)  
483.929 Million cell updates/sec

Title: US-10-822-254-10  
Perfect score: 555  
Sequence: 1 SQIPASQETVLVRKPLLLK.....NLVVNQSSDSGTSVSEN 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04.\*  
1: geneseqp1980s.\*  
2: geneseqp1990s.\*  
3: geneseqp2000s.\*  
4: geneseqp2001s.\*  
5: geneseqp2002s.\*  
6: geneseqp2003as.\*  
7: geneseqp2003bs.\*  
8: geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	545	98.2	284	2	AAR75494 Human dou
2	545	98.2	284	2	AAR75397 Human dou
3	545	98.2	491	2	AAR42175 Human MDM
4	545	98.2	491	2	AAR76696 Human MDM
5	545	98.2	491	2	AAR07887 Human MDM
6	545	98.2	491	2	AAR15463 Human MDM
7	545	98.2	491	2	AAR13380 Human MDM
8	545	98.2	491	2	AAR13600 Murine do
9	545	98.2	491	2	AAR48241 Human MDM
10	545	98.2	491	2	AAR57241 Human MDM
11	545	98.2	491	2	AAR42879 Amino aci
12	545	98.2	491	2	AAR42971 Amino aci
13	545	98.2	491	2	AAR94304 Human MDM
14	545	98.2	491	3	AAR96567 MDM2 onco
15	545	98.2	491	4	AAR48284 Human MDM
16	545	98.2	491	5	AAR22654 Human Rin
17	545	98.2	491	5	AAR22698 Human Rin
18	545	98.2	491	5	AAR25913 Human dou
19	545	98.2	491	5	AAR15376 Human Dm2
20	545	98.2	491	7	ADD21815 Human mdm
21	545	98.2	491	7	AD61562 Human Pro
22	545	98.2	491	8	ADL23893 Human E3
23	545	98.2	491	8	ADO52353 Human p53
24	545	98.2	491	8	ADP12593 Protein e
25	545	98.2	491	8	ADN71936 MDM2 prot

26	545	98.2	491	8	ADQ19417 Human sof
27	545	98.2	1171	4	AAR32421 Novel hum
28	528.5	95.2	216	3	AAB08846 A human M
29	519.5	93.6	522	7	ADJ95152 Novel NOV
30	519.5	93.6	522	7	ADJ95154 Novel NOV
31	485.5	87.5	489	2	AAR42176 Murine MD
32	485.5	87.5	489	2	AAR76697 Mouse MDM
33	485.5	87.5	489	2	AAR07888 Murine MD
34	485.5	87.5	489	2	AAR15464 Murine MD
35	485.5	87.5	489	2	AAR48242 Mouse MDM
36	485.5	87.5	489	2	AAR57246 Mouse MDM
37	485.5	87.5	489	2	AAR42997 Amino aci
38	485.5	87.5	489	2	AAR42972 Amino aci
39	485.5	87.5	489	2	AAR94305 Mouse MDM
40	485.5	87.5	489	5	AAR25914 Mouse dou
41	485.5	87.5	489	5	AAR57099 Mouse isc
42	485.5	87.5	489	5	AAR15375 Mouse Dm2
43	485.5	87.5	489	7	ADD21816 Mouse mdm
44	485.5	87.5	489	7	AD61560 Rat Prote
45	347	62.5	227	2	AAR75495 Human dou

## ALIGNMENTS

RESULT 1  
AAR75494  
ID AAR75494 standard; protein; 284 AA.  
XX  
AC AAR75494;  
XX  
DT 02-FEB-1996 (first entry)  
XX  
DE Human double minute 2 (hdm-2) antibody-binding region fragment 1.  
XX  
KW Human double minute gene 2; hdm-2; antibody binding region; antigen;  
KW cancer; sarcoma; rhabdomyosarcoma; diagnosis; immunoassay.  
XX  
OS Homo sapiens.  
XX  
PH Key Location/Qualifiers  
FT Region 1..284  
FT /note= "amino acids 1-284 of hdm-2 gene product"  
XX  
PN DE4339533-A1.  
XX  
PD 14-JUN-1995.  
XX  
PF 19-NOV-1993; 93DE-04339533.  
XX  
PR 19-NOV-1993; 93DE-04339533.  
XX  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
XX  
PI Zentgraf H, Klein R, Frey M, Martens R;  
XX  
DR WPI; 1995-216248/29.  
XX  
N-PSDB; AAQ92515.  
XX  
PT Detection of human double minute gene 2 (hdm-2) antibodies - by  
PT incubation with new hdm-2 or antibody-binding hdm-2 fragments; useful in  
PT the detection of specific cancers.  
XX  
PS Claim 11; Fig 1; 12pp; German.  
XX  
CC Fragments contg. amino acids 1-284, 58-284 and 58-491 of the hdm-2 (human  
CC double minute 2) gene product are claimed. The overlapping protein  
CC fragments contain binding regions for hdm-2- specific antibodies and are  
CC useful for identifying such antibodies in a claimed immunoassay method.  
CC The presence of anti-hdm-2 antibodies is diagnostic of certain forms of  
CC cancer, e.g. rhabdomyosarcoma  
XX  
SQ Sequence 284 AA;

Query Match 98.2%; Score 545; DB 2; Length 284;  
Best Local Similarity 98.2%; Pred. No. 1.9e-62;  
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVH 60  
DB 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDLLGDLFGVPSPSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 109  
DB 77 CSNDLLGDLFGVPSPSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 125

## RESULT 2

AAR75397  
ID AAR75397 standard; protein; 284 AA.

XX AC AAR75397;

XX DT 25-MAR-2003 (revised)  
XX DT 25-JAN-1996 (first entry)

XX DE Human double minute 2 (hdm-2) antibody-binding region fragment 1.  
XX KW Human double minute gene 2; hdm-2; antibody binding region; antigen;  
XX KW cancer; sarcoma; rhabdomyosarcoma; diagnosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
XX FT Region 1. .284  
XX FT /note= "amino acids 1-284 of hdm-2 gene product"

XX PN DE4345249-A1.

XX PD 24-MAY-1995.

XX PF 19-NOV-1993; 93DE-04345249.

XX PR 19-NOV-1993; 93DE-04339533.

XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX PI Zentgraf H, Klein R, Frey M, Martens R;

XX DR WPI; 1995-195167/26.

XX DR N-PSDB; AAQ87261.

XX PT New hdm-2 fragments contg. antibody binding region - used to detect  
XX PT specific antibodies for diagnosis of cancers, also new DNA sequences  
XX PT encoding them.

XX PS Claim 2; Fig 1; 11pp; German.

XX CC Fragments contg. amino acids 1-284, 58-284 and 58-491 of the hdm-2 (human  
XX CC double minute 2) gene product are claimed. The overlapping protein  
XX CC fragments contain binding regions for hdm-2- specific antibodies and are  
XX CC useful for identifying such antibodies. The presence of anti-hdm-2  
XX CC antibodies is diagnostic of certain forms of cancer, e.g.  
XX CC rhabdomyosarcoma. (Updated on 25-MAR-2003 to correct PF field.)

XX SQ Sequence 284 AA;

Query Match 98.2%; Score 545; DB 2; Length 284;  
Best Local Similarity 98.2%; Pred. No. 1.9e-62;  
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVH 60  
DB 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDLLGDLFGVPSPSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 109

DB 77 CSNDLLGDLFGVPSPSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 125

## RESULT 3

AAR42175  
ID AAR42175 standard; protein; 491 AA.

XX AC AAR42175;

XX DT 25-MAR-2003 (revised)  
XX DT 05-MAY-1994 (first entry)

XX DE Human MDM2.

XX KW p53 gene; tumour suppressor gene; regulation; cellular proliferation;  
XX KW cellular transformation; carcinoma; human; tumour; MDM2; inhibition;  
XX KW gene amplification.

XX OS Homo sapiens.

XX PN WO9320238-A2.

XX PD 14-OCT-1993.

XX PF 07-APR-1993; 93WO-US003199.

XX PR 07-APR-1992; 92US-00867840.

XX PR 23-JUN-1992; 92US-00903103.

XX PA (UYJO) UNIV JOHNS HOPKINS.

XX PI Burrell M, Hill DE, Kinzler KW, Vogelstein B;

XX DR WPI; 1993-336944/42.

XX DR N-PSDB; AAQ49891.

XX PT Diagnosing neoplasia from amplification of MDM2 gene - or elevated gene  
XX PT expression, also new DNA, MDM2 protein, antibodies and treatment of  
XX PT sarcoma by inhibiting MDM2 expression.

XX PS Claim 19; Fig 1; 75pp; English.

XX CC This sequence is encoded by the MDM2 gene. Amplification of the MDM2 gene  
XX CC is diagnostic of neoplasia or the potential for neoplasia. The protein  
XX CC encoded by this gene interacts with the product of the p53 gene. p53 is a  
XX CC tumour suppressor gene and encodes a protein which appears to be a member  
XX CC of a group of proteins which regulate normal cellular proliferation and  
XX CC suppression of cellular transformation. Inactivation of the p53 gene has  
XX CC been implicated in the formation, or progression of a wide variety of  
XX CC carcinoma. Polypeptides containing at least amino acids 13-41 of p53, or  
XX CC the DNA encoding these, may be used to inhibit the growth of tumour cells  
XX CC containing MDM2 gene amplification. (Updated on 25-MAR-2003 to correct PN  
XX CC field.)

XX SQ Sequence 491 AA;

Query Match 98.2%; Score 545; DB 2; Length 491;  
Best Local Similarity 98.2%; Pred. No. 4e-62;  
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVH 60  
DB 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDLLGDLFGVPSPSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 109

DB 77 CSNDLLGDLFGVPSPSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 125

## RESULT 4

AAR76696

ID AAR76696 standard; protein; 491 AA.

```

XX AAR76696;
XX 16-OCT-2003 (revised)
XX 01-NOV-1995 (first entry)
XX Human MDM2 protein.
XX MDM2; sarcoma; diagnostic; DNA probe.
XX Homo sapiens; (cell line CaCo-2).
XX US5420263-A.
XX 30-MAY-1995.
XX 07-APR-1993; 93US-00044619.
XX 07-APR-1992; 92US-00867840.
XX 23-JUN-1992; 92US-00903103.
XX (UYJO ) UNIV JOHNS HOPKINS.
XX Vogelstein B, Kinzler KW;
XX WPI; 1995-206312/27.
XX N-PSDB; AAQ94589.
XX New human MDM2 cDNA - used to develop prods. for use in the diagnosis and
XX treatment of tumours.
XX Claim 1; Col 23-26; 34pp; English.
XX The human MDM2 gene is genetically altered (i.e. amplified) in human
XX tumour cells. The human MDM2 protein binds to human p53 and allows the
XX cell to escape from p53-regulated growth. Detecting that the gene has
XX become amplified or detecting increased gene product expression (using
XX probes, proteins, antibodies and inhibitors) allows diagnosis and therapy
XX of cancers such as colorectal carcinoma, lung cancer and chronic
XX myelogenous leukaemia. (Updated on 16-OCT-2003 to standardise OS field)
XX
XX Sequence 491 AA;
XX
XX Query Match 98.2%; Score 545; DB 2; Length 491;
XX Best Local Similarity 98.2%; Pred. No. 4e-62;
XX Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTWKEVLVYLGOYIMTKRLYDEKQOHIVH 60
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTWKEVLVYLGOYIMTKRLYDEKQOHIVY 76
Qy 61 CSNDLLGDLFGVPSPSVKEHRKIYTMIVRNLVVNNQSSDSGTSVSEN 109
Db 77 CSNDLLGDLFGVPSPSVKEHRKIYTMIVRNLVVNNQSSDSGTSVSEN 125
XX
RESULT 5
AAW07887
ID AAW07887 standard; protein; 491 AA.
XX
AC AAW07887;
XX
XX 25-MAR-2003 (revised)
XX 28-JAN-1997 (first entry)
XX
XX Human MDM-2, involved in tumour-development.
XX p53; MDM-2; binding-inhibitor; identification; tumour; cancer; neoplasia;
XX antibody fusion protein; therapy.
XX Homo sapiens.
XX
XX Key Location/Qualifiers

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FT Modified-site 166..169
FT /label= phosphorylation_site
FT /note= "potential casein kinase II phosphorylation site"
FT Binding-site 181..185
FT /label= nuclear_localisation_signal
FT Modified-site 192..195
FT /label= phosphorylation_site
FT /note= "potential casein kinase II phosphorylation site"
FT Domain 223..274
FT /label= acid_activation_domain
FT Modified-site 269..272
FT /label= phosphorylation_site
FT /note= "potential casein kinase II phosphorylation site"
FT Modified-site 290..293
FT /label= phosphorylation_site
FT /note= "potential casein kinase II phosphorylation site"
FT Domain 305..322
FT /label= metal_binding_site
FT Domain 461..478
FT /label= metal_binding_site
XX US5550023-A.
XX 27-AUG-1996.
XX 18-MAY-1994; 94US-00245500.
XX 07-APR-1992; 92US-00867840.
XX 23-JUN-1992; 92US-00903103.
XX 07-APR-1993; 93US-00044619.
XX (UYJO ) UNIV JOHNS HOPKINS.
XX Vogelstein B, Kinzler KW;
XX WPI; 1996-401591/40.
XX N-PSDB; AAT45151.
XX Identification of cpds. interfering with human MDM2/p53 binding - useful
XX as therapeutic agents to treat human neoplastic cells.
XX Claim 26; Col 25-28; 36pp; English.
XX
XX AAW07887 represents human MDM-2 derived from a human colon carcinoma cell
XX line, CaCo-2, cDNA library. The MDM-2 protein is used in a method for
XX identifying compounds that interfere with the binding of p53 and MDM-2.
XX In binding the p53 protein, the MDM-2 protein releases a cell from p53-
XX regulated growth, allowing cancers to develop. Therefore compounds
XX identified as interfering with the binding of MDM-2 to p53 are
XX potentially useful in the treatment of human neoplastic cells. In the
XX method pref. one or both of the proteins is a fusion protein esp. with an
XX antibody or antibody fragment which aids separation and identification.
XX (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 491 AA;
XX
XX Query Match 98.2%; Score 545; DB 2; Length 491;
XX Best Local Similarity 98.2%; Pred. No. 4e-62;
XX Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTWKEVLVYLGOYIMTKRLYDEKQOHIVH 60
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTWKEVLVYLGOYIMTKRLYDEKQOHIVY 76
Qy 61 CSNDLLGDLFGVPSPSVKEHRKIYTMIVRNLVVNNQSSDSGTSVSEN 109
Db 77 CSNDLLGDLFGVPSPSVKEHRKIYTMIVRNLVVNNQSSDSGTSVSEN 125
XX
RESULT 6
AAW15463
ID AAW15463 standard; protein; 491 AA.
XX

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AC AAW15463;
XX
XX
DT 25-MAR-2003 (revised)
DT 18-JUN-1997 (first entry)
XX
XX Human MDM2.
DE
XX
XX Human; MDM2 protein; antibody; detection; cancer; diagnosis;
XX p53-regulated growth.
XX
XX Homo sapiens.
XX
XX US5618921-A.
XX
XX 08-APR-1997.
XX
XX 17-FEB-1995; 95US-00390479.
XX
XX 07-APR-1992; 92US-00867840.
PR 23-JUN-1992; 92US-00903103.
PR 07-APR-1993; 93US-00044619.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Vogelstein B, Kinzler KW, Burrell M, Hill DE;
XX
XX WPI; 1997-225474/20.
DR N-PSDB; AAT66410.
XX
XX Antibodies specific for human MDM2 protein - for diagnosis of cancer.
XX
XX Claim 1; Col 19-24; 35pp; English.
XX
XX This sequence represents the human MDM2 protein. Antibodies that
XX specifically bind to human MDM2 protein may be used for detecting
XX elevated expression of the MDM2 gene in a human tissue or body fluid
XX sample, esp. for cancer diagnosis. The antibodies may be used to
XX interfere with the binding of p53 to MDM2. Elevated levels of MDM2 appear
XX to sequester p53 and allow the cell to escape from p53-regulated growth.
XX (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 491 AA;
SQ
Query Match 98.2%; Score 545; DB 2; Length 491;
Best Local Similarity 98.2%; Pred. No. 4e-62;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVH 60
DB 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVY 76
QY 61 CSNDLLGDLFGVPSFSVKEHRIYTMIRNLVVVNQQESSDSGTSVSEN 109
DB 77 CSNDLLGDLFGVPSFSVKEHRIYTMIRNLVVVNQQESSDSGTSVSEN 125
RESULT 7
AAW13380
ID AAW13380 standard; protein; 491 AA.
XX
XX AAW13380;
AC
XX
XX 25-MAR-2003 (revised)
DT 05-JUN-1997 (first entry)
XX
XX Human MDM2 protein.
DE
XX Human; MDM2; CaCo-2; colonic; carcinoma; probe; detection; amplification;
XX elevation; expression; diagnosis; neoplasia; neoplastic transformation;
XX sarcoma; colorectal; lung cancer; chronic myelogenous leukaemia.
XX
XX Homo sapiens.
XX

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PN US5606044-A.
XX
XX 25-FEB-1997.
XX
XX 17-FEB-1995; 95US-00390546.
XX
XX 07-APR-1992; 92US-00867840.
PR 23-JUN-1992; 92US-00903103.
PR 07-APR-1993; 93US-00044619.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Kinzler KW, Vogelstein B, Hill DE, Burrell M;
XX
XX WPI; 1997-153623/14.
DR N-PSDB; AAT62065.
XX
XX Detection of amplification of human MDM2 gene - useful for diagnosis of
XX neoplasia or potential neoplastic transformation.
XX
XX Example 1; Col 21-24; 35pp; English.
XX
XX The present sequence is the human MDM2 protein, the cDNA for which was
XX isolated from a human CaCo-2 colonic carcinoma cell cDNA library using a
XX murine MDM2 cDNA probe. The MDM2 cDNA can be used as a probe to detect
XX the amplification or elevated expression of a human MDM2 gene, which is
XX diagnostic of neoplasia or the potential for neoplastic transformation,
XX useful for the detection of, e.g. sarcomas, colorectal carcinoma, lung
XX cancer and chronic myelogenous leukaemia. (Updated on 25-MAR-2003 to
XX correct PF field.)
XX
XX Sequence 491 AA;
SQ
Query Match 98.2%; Score 545; DB 2; Length 491;
Best Local Similarity 98.2%; Pred. No. 4e-62;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVH 60
DB 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVY 76
QY 61 CSNDLLGDLFGVPSFSVKEHRIYTMIRNLVVVNQQESSDSGTSVSEN 109
DB 77 CSNDLLGDLFGVPSFSVKEHRIYTMIRNLVVVNQQESSDSGTSVSEN 125
RESULT 8
AAW13600
ID AAW13600 standard; protein; 491 AA.
XX
XX AAW13600;
AC
XX
XX 16-JAN-1998 (first entry)
DT
XX
XX Murine double minute 2 protein sequence.
DE
XX
XX Mouse; Mdm2; murine double minute; phosphoprotein; binding; modulation;
XX tumour suppressor; p53; oncogene; cell cycle arrest; p107; antagonist;
XX inhibition; transcription factor; adenocarcinoma; colon; cancer; breast;
XX lung; stomach; myeloid leukaemia; lymphoma; hyperproliferative;
XX resection.
XX
XX Mus musculus.
OS
XX
XX WO9709343-A2.
PN
XX
XX 13-MAR-1997.
PD
XX
XX 02-SEP-1996; 96WO-FR001340.
PF
XX
XX 04-SEP-1995; 95FR-00010331.
PR
XX
XX (RHON ) RHONE POULENC RORER SA.
PA

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(INRM ) INST NAT SANTE & RECH MEDICALE.  
Tocque B, Dubs-Poterszman M, Wasylyk B;  
WPI; 1997-192837/17.  
N-PSDB; AAT61637.  
Treating cancer with antagonist of oncogenic activity of protein Mdm2 -  
nucleic acid encoding an antagonist, also viral vectors contg. this  
nucleic acid.  
Claim 2; Page 26-30; 43pp; French.  
This is the amino acid sequence of the mouse Mdm2 (murine double minute-  
2) protein, a 90 kD phosphoprotein which binds and modulates the activity  
of the tumour suppressor protein p53. It has now been shown that the mdm2  
protein itself has oncogenic properties, especially in a p53-null  
background. Mdm2 is observed to unblock cell cycle arrest in G1 caused by  
over-expression of the p107 protein. This is especially done by the  
region covering amino acid 1-134. The invention therefore relates to  
antagonists able to inhibit the oncogenic activity of mdm2. These include  
fragments of the p53 protein, especially amino acids 1-52, 1-41, 6-41, 16  
-25 or 18-23 (AAW13602-6), or fragments of transcription factors e.g.  
TFII, TBP or TAP250, which bind amino acids 1-134 of mdm2. Other  
inhibitors include compounds which disrupt binding to region 135-491 of  
mdm2, e.g. RD, L5 or the transcription factor E2F. The antagonists are  
used to treat e.g. adenocarcinoma of the colon; cancer of the breast,  
lung or stomach; myeloid leukaemia; B cell lymphoma, or other  
hyperproliferative conditions such as restenosis

XX PA (INRM ) INST NAT SANTE & RECH MEDICALE.  
XX Pi Tocque B, Dubs-Poterszman M, Wasylyk B;  
XX DR WPI; 1997-192837/17.  
XX DR N-PSDB; AAT61637.  
XX DR Treating cancer with antagonist of oncogenic activity of protein Mdm2 -  
XX PT nucleic acid encoding an antagonist, also viral vectors contg. this  
XX PT nucleic acid.  
XX PS Claim 2; Page 26-30; 43pp; French.  
XX XX This is the amino acid sequence of the mouse Mdm2 (murine double minute-  
XX CC 2) protein, a 90 kD phosphoprotein which binds and modulates the activity  
XX CC of the tumour suppressor protein p53. It has now been shown that the mdm2  
XX CC protein itself has oncogenic properties, especially in a p53-null  
XX CC background. Mdm2 is observed to unblock cell cycle arrest in G1 caused by  
XX CC over-expression of the p107 protein. This is especially done by the  
XX CC region covering amino acid 1-134. The invention therefore relates to  
XX CC antagonists able to inhibit the oncogenic activity of mdm2. These include  
XX CC fragments of the p53 protein, especially amino acids 1-52, 1-41, 6-41, 16  
XX CC -25 or 18-23 (AAW13602-6), or fragments of transcription factors e.g.  
XX CC TFII, TBP or TAP250, which bind amino acids 1-134 of mdm2. Other  
XX CC inhibitors include compounds which disrupt binding to region 135-491 of  
XX CC mdm2, e.g. RD, L5 or the transcription factor E2F. The antagonists are  
XX CC used to treat e.g. adenocarcinoma of the colon; cancer of the breast,  
XX CC lung or stomach; myeloid leukaemia; B cell lymphoma, or other  
XX CC hyperproliferative conditions such as restenosis

XX SQ Sequence 491 AA;  
Query Match 98.2%; Score 545; DB 2; Length 491;  
Best Local Similarity 98.2%; Pred. No. 4e-62;  
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SQIPASQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYVLGYIMTKRLYDEKQHIVH 60  
Db 17 SQIPASQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYVLGYIMTKRLYDEKQHIVY 76  
Qy 61 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 109  
Db 77 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 125

RESULT 9  
AAW48241  
ID AAW48241 standard; protein; 491 AA.  
AC AAW48241;  
DT 18-JUN-1998 (first entry)  
XX Human MDM2.  
XX Human; MDM2; hMDM2; tumour; cancer; diagnosis; neoplastic disease;  
XX KW sarcoma; liposarcoma; malignant fibrous histiocytoma; osteosarcoma.  
XX OS Homo sapiens.  
XX PN US5736338-A.  
XX PD 07-APR-1998.  
XX PF 17-FEB-1995; 95US-00390517.  
XX PR 07-APR-1992; 92US-00867840.  
XX PR 23-JUN-1992; 92US-00903103.  
XX PR 07-APR-1993; 93US-00044619.  
XX PA (UYJO ) UNIV JOHNS HOPKINS.  
XX Pi Vogelstein B, Kinzler KW, Hill DE, Burrell M;  
XX DR WPI; 1998-321574/28.  
XX DR N-PSDB; AAV28876.  
XX PT Inhibiting growth of tumour cells having MDM2 gene amplification - with  
XX PT p53 protein fragment.  
XX PS Claim 1; Col 23-28; 40pp; English.  
XX CC A method has been developed for inhibiting the growth of tumour cells  
XX CC containing a human MDM2 gene amplification. The method comprises treating  
XX CC the tumour cells with a DNA molecule that expresses a polypeptide capable  
XX CC of binding to human MDM2 protein. The present sequence represents human  
XX CC MDM2 protein. The present invention describes three preferred  
XX CC polypeptides for binding human MDM2: (1) the polypeptide comprises amino

XX DR WPI; 1998-239206/21.  
XX DR N-PSDB; AAV20549.  
XX PT Cancer diagnosis - by determination of MDM2 protein.  
XX PS Claim 1; Col 25-28; 35pp; English.  
XX XX The present sequence represents human MDM2 (hMDM2) which is used in the  
XX CC method of the present invention. The present invention describes a method  
XX CC for diagnosing a neoplastic disease caused by overexpression of MDM2  
XX CC protein. The method comprises detecting an elevated cellular amount of  
XX CC this protein. The method is useful for the diagnosis of sarcoma,  
XX CC especially liposarcoma, malignant fibrous histiocytoma or osteosarcoma  
XX SQ Sequence 491 AA;  
Query Match 98.2%; Score 545; DB 2; Length 491;  
Best Local Similarity 98.2%; Pred. No. 4e-62;  
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SQIPASQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYVLGYIMTKRLYDEKQHIVH 60  
Db 17 SQIPASQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYVLGYIMTKRLYDEKQHIVY 76  
Qy 61 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 109  
Db 77 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 125

RESULT 10  
AAW57241  
ID AAW57241 standard; protein; 491 AA.  
AC AAW57241;  
DT 10-AUG-1998 (first entry)  
XX Human MDM2 protein.  
XX Human; p53; MDM2; tumour; growth inhibition; amplification;  
XX KW malignant fibrous histiocytoma; liposarcoma.  
XX OS Homo sapiens.  
XX PN US5756455-A.  
XX PD 26-MAY-1998.  
XX PF 17-FEB-1995; 95US-00390515.  
XX PR 07-APR-1992; 92US-00867840.  
XX PR 23-JUN-1992; 92US-00903103.  
XX PR 07-APR-1993; 93US-00044619.  
XX PA (UYJO ) UNIV JOHNS HOPKINS.  
XX Pi Vogelstein B, Kinzler KW;  
XX DR WPI; 1998-321574/28.  
XX DR N-PSDB; AAV28876.  
XX PT Inhibiting growth of tumour cells having MDM2 gene amplification - with  
XX PT p53 protein fragment.  
XX PS Claim 1; Col 23-28; 40pp; English.  
XX CC A method has been developed for inhibiting the growth of tumour cells  
XX CC containing a human MDM2 gene amplification. The method comprises treating  
XX CC the tumour cells with a DNA molecule that expresses a polypeptide capable  
XX CC of binding to human MDM2 protein. The present sequence represents human  
XX CC MDM2 protein. The present invention describes three preferred  
XX CC polypeptides for binding human MDM2: (1) the polypeptide comprises amino

CC acids 1-50 of p53 (see AAW57240); (2) the polypeptide comprises amino  
 CC acids 13-41 of p53 (see AAW57240) and at least none additional p53  
 CC residues on the N- or C-terminal side, provided that the polypeptide  
 CC lacks the homooligomerisation domain of p53; (3) the polypeptide  
 CC comprises amino acids 13-41 of p53 (see AAW57241) and at least nine  
 CC additional p53 residues on the N- or C-terminal side, provided that the  
 CC polypeptide lacks amino acids 138-393 of p53. Some malignant fibrous  
 CC histiocytomas and liposarcomas have an MDM2 gene amplification, so  
 CC detection of increased expression of MDM2 gene products indicates  
 CC tumorigenesis  
 XX  
 SQ Sequence 491 AA;  
 Query Match 98.2%; Score 545; DB 2; Length 491;  
 Best Local Similarity 98.2%; Pred. No. 4e-62;  
 Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYLGYIMTKRLYDEKQOHIVH 60  
 Db 17 SQIPASQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYLGYIMTKRLYDEKQOHIV 76  
 Qy 61 CSNDLLGDLFGVPSFVSKEHRKIYTMIRNLVVVNQOESSDSTSVSEN 109  
 Db 77 CSNDLLGDLFGVPSFVSKEHRKIYTMIRNLVVVNQOESSDSTSVSEN 125

RESULT 11  
 AAW42879  
 ID AAW42879 standard; protein; 491 AA.  
 XX  
 AC AAW42879;  
 XX  
 DT 30-APR-1998 (first entry)  
 XX  
 DE Amino acid sequence of human MDM2.  
 XX  
 KW MDM2; tumour; diagnosis; neoplasia; DNA binding protein; p53 polypeptide;  
 KW binding; tumour cell; p53-regulated growth; inhibition;  
 KW anti-cancer agent.  
 XX  
 OS Homo sapiens.  
 XX  
 FN US5708136-A.  
 XX  
 PD 13-JAN-1998.  
 XX  
 PF 17-FEB-1995; 95US-00390516.  
 XX  
 PR 07-APR-1992; 92US-00867840.  
 PR 23-JUN-1992; 92US-00903103.  
 PR 07-APR-1993; 93US-00044619.  
 XX  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 PI Vogelstein B, Kinzler KW, Burrell M, Hill DE;  
 XX  
 WPI; 1998-100408/09.  
 XX  
 PT Human MDM2 binding polypeptide - comprises fragments of p53, useful in re  
 PT -establishing p53-regulated growth control in cells over-expressing MDM2.  
 XX  
 PS Disclosure; Col 23-28; 41pp; English.  
 XX  
 CC The present sequence represents human MDM2. The MDM2 gene is amplified in  
 CC some human tumours. The amplification of this gene is diagnostic of  
 CC neoplasia or its potential. It is speculated that the MDM2 protein is a  
 CC potential DNA binding protein that functions in the modulation of  
 CC expression of other genes and, when present in excess, interferes with  
 CC normal constraints on cell growth. A cell containing three recombinant  
 CC DNA constructs was produced. These constructs encode an MDM2 protein  
 CC fused to a sequence-specific DNA binding domain, a p53 polypeptide fused  
 CC to a transcriptional activation domain, and a reporter gene downstream  
 CC from a DNA element which is recognised by the sequence-specific DNA-

CC binding domain. The cell is used to identify a compound which interferes  
 CC with the binding of MDM2 and p53. Since MDM2 is overexpressed in tumour  
 CC cells and since binding of MDM2 to p53 appears to allow tumour cells to  
 CC escape from p53-regulated growth, compounds that inhibit such binding  
 CC would be useful as anti-cancer agents  
 XX  
 SQ Sequence 491 AA;  
 Query Match 98.2%; Score 545; DB 2; Length 491;  
 Best Local Similarity 98.2%; Pred. No. 4e-62;  
 Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYLGYIMTKRLYDEKQOHIVH 60  
 Db 17 SQIPASQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYLGYIMTKRLYDEKQOHIV 76  
 Qy 61 CSNDLLGDLFGVPSFVSKEHRKIYTMIRNLVVVNQOESSDSTSVSEN 109  
 Db 77 CSNDLLGDLFGVPSFVSKEHRKIYTMIRNLVVVNQOESSDSTSVSEN 125

RESULT 12  
 AAW42971  
 ID AAW42971 standard; protein; 491 AA.  
 XX  
 AC AAW42971;  
 XX  
 DT 29-APR-1998 (first entry)  
 XX  
 DE Amino acid sequence of human MDM2.  
 XX  
 KW MDM2; tumour; diagnosis; neoplasia; DNA binding protein; p53 polypeptide;  
 KW binding; tumour cell; p53-regulated growth; inhibition;  
 KW anti-cancer agent.  
 XX  
 OS Homo sapiens.  
 XX  
 FN US5702903-A.  
 XX  
 PD 30-DEC-1997.  
 XX  
 PF 13-NOV-1995; 95US-00557393.  
 XX  
 PR 07-APR-1992; 92US-00867840.  
 PR 23-JUN-1992; 92US-00903103.  
 PR 07-APR-1993; 93US-00044619.  
 PR 18-MAY-1994; 94US-00245500.  
 XX  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 PI Vogelstein B, Kinzler KW;  
 XX  
 WPI; 1998-076411/07.  
 XX  
 N-PSDB; AAV03607.  
 XX  
 PT Cell containing reporter construct containing human MDM2 and p53 genes -  
 PT for identifying compounds that interfere with binding of human MDM2 to  
 PT human p53, useful as anti-cancer agents.  
 XX  
 PS Disclosure; Coulms 22-28; 37pp; English.  
 XX  
 CC The present sequence represents human MDM2. The MDM2 gene is amplified in  
 CC some human tumours. The amplification of this gene is diagnostic of  
 CC neoplasia or its potential. It is speculated that the MDM2 protein is a  
 CC potential DNA binding protein that functions in the modulation of  
 CC expression of other genes and, when present in excess, interferes with  
 CC normal constraints on cell growth. A cell containing three recombinant  
 CC DNA constructs was produced. These constructs encode an MDM2 protein  
 CC fused to a sequence-specific DNA binding domain, a p53 polypeptide fused  
 CC to a transcriptional activation domain, and a reporter gene downstream  
 CC from a DNA element which is recognised by the sequence-specific DNA-  
 CC binding domain. The cell is used to identify a compound which interferes  
 CC with the binding of MDM2 and p53. Since MDM2 is overexpressed in tumour

CC cells and since binding of MDM2 to p53 appears to allow tumour cells to  
 CC escape from p53-regulated growth, compounds that inhibit such binding  
 CC would be useful as anti-cancer agents

XX SQ Sequence 491 AA;

Query Match 98.2%; Score 545; DB 2; Length 491;

Best Local Similarity 98.2%; Pred. No. 4e-62; Mismatches 0; Indels 0; Gaps 0;  
 Matches 107; Conservative 2;

Qy 1 SQIPASQETLVRPKPLLLKLLKSVGAQKQDTYTMKEVLYYLGOYIMTKRLYDEKQOHIVH 60  
 Db 17 SQIPASQETLVRPKPLLLKLLKSVGAQKQDTYTMKEVLYYLGOYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 109  
 Db 77 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 125

#### RESULT 13

ID AAW94304 standard; protein; 491 AA.

XX AAW94304;

DT 13-APR-1999 (first entry)

XX Human MDM2.

XX Human; MDM2; p53; tumorigenesis; growth regulation; diagnosis;  
 KW malignant fibrous histiocytoma; MFH; liposarcoma.

XX Homo sapiens.

XX US5858976-A.

XX 12-JAN-1999.

XX 14-FEB-1997; 97US-00801718.

XX 07-APR-1992; 92US-00867840.

XX 23-JUN-1992; 92US-00903103.

XX 07-APR-1993; 93US-00044619.

XX 17-FEB-1995; 95US-00390515.

XX (UYJO ) UNIV JOHNS HOPKINS.

XX Kinzler KW, Vogelstein B;

XX WPI; 1999-152105/13.

XX N-PSDB; AAX03947.

XX Inhibiting growth of tumour cells having MDM2 gene amplification - with  
 PT MDM2-binding p53 fragment.

XX Claim 1; Col 23-28; 41pp; English.

XX The present invention describes: (1) a method for inhibiting the growth  
 CC of tumour cells which contain a human MDM2 gene amplification, comprising  
 CC administering to the cells a DNA molecule that expresses a polypeptide  
 CC consisting of a portion of p53 i.e. amino acids 13-41 of the 64 amino  
 CC acid sequence given in AAW94303, the polypeptide being capable of binding  
 CC to human MDM2 (the present sequence); (2) a method as in (1) where the  
 CC polypeptide lacks the homo-oligomerisation domain of p53; and (3) a  
 CC method as in (1) where the polypeptide lacks amino acids 138-393 of p53.  
 CC The method is useful for treating the following tumour types which have a  
 CC MDM2 gene amplification: M-7 malignant fibrous histiocytoma (MFH), M-20  
 CC MFH, L-9 liposarcoma, KL7 liposarcoma, KL28 liposarcoma, and OSA-CL MFH  
 CC liposarcoma, and OSA-CL MFH

XX Sequence 491 AA;

Query Match

98.2%; Score 545; DB 2; Length 491;

Best Local Similarity 98.2%; Pred. No. 4e-62; Mismatches 0; Indels 0; Gaps 0;  
 Matches 107; Conservative 2;

Qy 1 SQIPASQETLVRPKPLLLKLLKSVGAQKQDTYTMKEVLYYLGOYIMTKRLYDEKQOHIVH 60  
 Db 17 SQIPASQETLVRPKPLLLKLLKSVGAQKQDTYTMKEVLYYLGOYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 109  
 Db 77 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 125

#### RESULT 14

AAAY96567

ID AAY96567 standard; protein; 491 AA.

XX AC AAY96567;

DT 12-SEP-2000 (first entry)

XX MDM2 oncoprotein.

XX hEST2; telomerase; catalytic subunit; reverse transcriptase; life-span;  
 KW retinoblastoma; p53; tumour suppressor; inhibitor; arteriosclerosis;  
 KW proliferation; immortal; tumour therapy; macular degeneration; activator;  
 KW INK4; MDM2; oncoprotein.

XX Homo sapiens.

XX W0200031238-A2.

XX 02-JUN-2000.

XX 24-NOV-1999; 99WO-US027907.

XX 25-NOV-1998; 98US-0109891P.

XX 17-FEB-1999; 99US-0120549P.

XX (GENE-) GENETICA INC.

XX Hannon GJ, Beach DH;

XX WPI; 2000-400055/34.

XX N-PSDB; AAA29389.

XX New method for increasing the proliferative capacity of cell lines  
 PT comprises administering agents reversibly activating telomerase activity  
 PT and reversibly inactivating Rb/INK4 and/or p53 pathways useful in  
 PT treating age related diseases.

XX Claim 5; Page 120; 123pp; English.

XX The invention concerns methods and reagents for extending the life-span,  
 CC e.g. the number of mitotic divisions, of a cell. The method relies on  
 CC activation of a telomerase activity and inhibition of one or both of a  
 CC retinoblastoma (Rb)/INK4 pathway or a p53 pathway. Phosphorylation of Rb  
 CC by cyclin-dependent kinases, cdk4 and cdk6, releases the cells into the  
 CC division cycle. Binding of INK4 family members, e.g. the tumour  
 CC suppressor p16INK4a, inhibits kinase activity and results in growth  
 CC arrest. Rb inactivators can selectively and reversibly inactivate an  
 CC Rb/INK4 pathway, especially an Rb/p16INK4a pathway. The oncoprotein MDM2  
 CC is a cellular inhibitor of Rb/E2F function and the p53 tumour suppressor  
 CC can also be used in the methods. Other molecules which can be used  
 CC include cdk4 or cdk6 mutants. In particular, a cdk4 mutant is one which  
 CC differs from at one or more of residues K22, R24, H95 and/or D97.  
 CC Additional constructs include a papilloma virus E7 protein, or other  
 CC viral oncoprotein which bypasses Rb and/or p53. Antisense constructs of  
 CC the Rb and p16INK4a genes may also be used. The methods are useful for  
 CC increasing the proliferative capacity of cells. The cells are  
 CC subsequently of use in pharmaceutical and cosmetic preparations used to  
 CC treat conditions related to (premature) ageing, e.g. macular degeneration  
 CC and arteriosclerosis. The cells can also be used to replace tumour cell  
 CC lines in vitro and for studies on biochemical and physiological aspects

CC of growth and differentiation. Long lived (immortal) cells could also be  
 CC of use in the production of normal or genetically engineered  
 CC biotechnology products  
 XX Sequence 491 AA;

Query Match 98.2%; Score 545; DB 3; Length 491;  
 Best Local Similarity 98.2%; Pred. No. 4e-62;  
 Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVPRPKPLLLKLLKSVGAQKDTYTMKEVLYLGGYIMTKRLYDEKQOHIV 60  
 Db 17 SQIPASEQETLVPRPKPLLLKLLKSVGAQKDTYTMKEVLYLGGYIMTKRLYDEKQOHIV 76

QY 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 109  
 Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 125

RESULT 15  
 AAB48284  
 ID AAB48284 standard; protein; 491 AA.

XX AAB48284;  
 AC 02-APR-2001 (first entry)  
 DT Human MDM2 protein.  
 DE S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; ZF;  
 KW CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;  
 KW Bad; Bcl-2; tumour; cytosstatic.  
 XX Homo sapiens.

XX WO200075184-A1.  
 PN 14-DEC-2000.  
 PD 05-JUN-2000; 2000WO-US015449.  
 PF 04-JUN-1999; 99US-0137494P.

XX (UYVA ) UNIV YALE.  
 XX Zhang H, Tsvetkov LM, Kondo T;  
 PI WPI; 2001-061703/07.  
 XX N-PSDB; AAC84596.  
 DR Modulating polypeptide levels in a cell, diagnosing and treating tumor,  
 PT involves altering levels of proteins such as S-phase kinase associated  
 PT proteins 1, 2 and cullin/CDC53 proteins.  
 XX Claim 5; Page 93-95; 162pp; English.

XX The invention relates to methods of altering the polypeptide levels in a  
 CC cell, using proteins selected from S-phase kinase associated proteins 1  
 CC and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the  
 CC cullin/ CDC53 family of proteins). The method is useful for altering the  
 CC level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2  
 CC polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for  
 CC detecting tumours, and in monitoring tumor treatment in a mammal. Agents  
 CC that modulate interactions between SKP and target proteins are useful for  
 CC treating tumours  
 XX Sequence 491 AA;

Query Match 98.2%; Score 545; DB 4; Length 491;  
 Best Local Similarity 98.2%; Pred. No. 4e-62;  
 Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVPRPKPLLLKLLKSVGAQKDTYTMKEVLYLGGYIMTKRLYDEKQOHIV 60

Db 17 SQIPASEQETLVPRPKPLLLKLLKSVGAQKDTYTMKEVLYLGGYIMTKRLYDEKQOHIV 76  
 QY 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 109  
 Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 125

Search completed: January 27, 2005, 18:06:16  
 Job time : 81.8 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 27, 2005, 17:52:56 ; Search time 19.8 Seconds  
(without alignments)  
529.678 Million cell updates/sec

Title: US-10-822-254-10  
Perfect score: 555  
Sequence: 1 SQIPASEQETLVRPKPLLLK.....NLVVNQESSDSGTSVSEN 109

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	545	98.2	491	1 S24354	p53-binding protei
2	485.5	87.5	489	2 S15349	mdm2 protein - mou
3	274.5	49.5	489	2 S71955	MDM2-like p53-bind
4	83	15.0	685	1 SXBPT4	NAD+-protein ADP-r
5	83	15.0	698	1 S31630	NAD+-protein ADP-r
6	83	15.0	698	1 S31714	NAD+-protein ADP-r
7	72.5	13.1	565	2 S52682	hypothetical prote
8	72.5	13.1	2833	2 A43360	inositol 1,4,5-tri
9	72	13.0	967	2 A64710	type III restricti
10	71.5	12.9	514	2 D85069	hypothetical prote
11	70.5	12.7	467	2 T58448	hypothetical prote
12	70.5	12.7	838	2 I45557	eyeless, long form
13	70	12.6	969	2 E71810	type III restricti
14	69.5	12.5	709	2 E64213	DNA topoisomerase
15	68	12.3	369	2 F90220	conserved hypothet
16	67.5	12.2	401	2 F90288	hypothetical prote
17	67.5	12.2	422	2 T26334	hypothetical prote
18	67	12.1	176	2 J01813	B19R protein - vac
19	67	12.1	181	2 S75415	probable ribosomal
20	67	12.1	206	1 XUBVMC	methylated-DNA-(pr
21	67	12.1	261	2 H71680	exodeoxyribonuclea
22	67	12.1	1145	2 S55600	single-stranded DN
23	66	11.9	908	2 C70168	DNA polymerase I (
24	66	11.9	1074	2 G96504	probable En/Spm-li
25	65.5	11.8	331	2 B84938	flagellar motor sw
26	65.5	11.8	425	2 T50184	mammalian swi/snf
27	65.5	11.8	447	2 I64002	sodium-translocati
28	65.5	11.8	517	2 S32169	hypothetical prote
29	65.5	11.8	525	2 T15185	hypothetical prote

30	65	11.7	134	2	G69382	response regulator
31	65	11.7	260	2	T28182	hypothetical prote
32	64.5	11.6	277	2	A10589	conserved hypothet
33	64.5	11.6	339	2	A90395	1-aminocyclopropan
34	64.5	11.6	366	2	T07827	hypothetical prote
35	64.5	11.6	380	2	T32112	probable membrane
36	64.5	11.6	547	2	S64332	hypothetical prote
37	64.5	11.6	593	2	E81277	hypothetical prote
38	64.5	11.6	649	2	C81275	toxin secretion AT
39	64.5	11.6	704	2	H82381	DNA-directed RNA p
40	64.5	11.6	1292	2	F64237	exodeoxyribonuclea
41	64	11.5	286	2	B97743	ct244 hypothetical
42	64	11.5	346	2	G72094	CT244 hypothetical
43	64	11.5	346	2	G86528	conserved hypothet
44	64	11.5	346	2	B81574	1-aminocyclopropan
45	64	11.5	488	2	T47943	

## ALIGNMENTS

## RESULT 1

S24354  
p53-binding protein mdm2 - human  
N:Alternate names: mdm-2 oncogene; mouse double minute 2 homolog; p53-associated phospho  
N:Contains: p53-binding protein mdm2, splice form A  
C:Species: Homo sapiens (man)  
C:Date: 17-Mar-2000 #sequence revision 17-Mar-2000 #text\_change 17-Mar-2000  
C:Accession: S24354; S57338; G02026  
R:Oliner, J.D.; Kinzler, K.W.; Meltzer, P.S.; George, D.L.; Vogelstein, B.  
Nature 358, 80-83, 1992  
A:Title: Amplification of a gene encoding a p53-associated protein in human sarcomas.  
A:Reference number: S24354; MUID:92310576; PMID:1614537  
A:Accession: S24354  
A:Molecule type: mRNA  
A:Residues: 1-491 <OLI>  
A:Cross-references: EMBL:Z12020; NID:935211; PIDN:CAA78055.1; PID:G935212  
R:Zauberman, A.; Flusberg, D.; Haupt, Y.; Barak, Y.; Oren, M.  
Nucleic Acids Res. 23, 2584-2592, 1995  
A:Title: A functional p53-responsive intronic promoter is contained within the human mdm  
A:Reference number: S57338; MUID:95380270; PMID:7651818  
A:Accession: S57338  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-16, 'P', 18-24 <ZAU>  
A:Cross-references: EMBL:U28935; NID:G904033; PIDN:AAA82237.1; PID:G904034  
R:Lunec, J.  
submitted to the EMBL Data Library, August 1995  
A:Description: Multiple alternate spliced mdm2 transcripts with loss of p53 binding doma  
A:Reference number: G09070  
A:Accession: G02026  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-27,223-491 <LUN>  
A:Cross-references: EMBL:U33199; NID:992676; PIDN:AAA75514.1; PID:G992677  
A:Experimental source: splice form A  
C:Genetics:  
A:Gene: GDB:MDM2  
A:Cross-references: GDB:250456; OMIM:164785  
A:Map position: 12q14.3-12q15  
C:Superfamily: human p53-binding protein mdm2  
C:Keywords: alternative splicing; oncogene; phosphoprotein  
F:1-491/Product: p53-binding protein mdm-2 #status predicted <MAT1>  
F:1-27,223-491/Product: p53-binding protein mdm-2, splice form A #status predicted <MAT2>

Query Match 98.2%; Score 545; DB 1; Length 491;

Best Local Similarity 98.2%; Pred. No. 5e-48;  
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKQDYTWKEVLYLGGQYIMTKRLYDEKQOHLVH 60  
|||||  
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKQDYTWKEVLYLGGQYIMTKRLYDEKQOHLVY 76  
|||||

```
Qy 61 CSNDLLGLDFGVPSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 109
|||||
Db 77 CSNDLLGLDFGVPSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 125
|||||

RESULT 2
mdm2 protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S15349
R:Fakhrazadeh, S.S.; Trusko, S.P.; George, D.L.
EMBO J. 10, 1565-1569, 1991
A:Title: Tumorigenic potential associated with enhanced expression of a gene that is am
A:Reference number: S15349; MUID:91224107; PMID:2026149
A:Accession: S15349
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-489 <FAK>
A:Cross-references: UNIPROT:P23804; EMBL:X58876; NID:g53038; PIDN:CAA41684.1; PID:g53039
C:Genetics:
A:Gene: mdm2
C:Superfamily: human p53-binding protein mdm2

Query Match 87.5%; Score 485.5; DB 2; Length 489;
Best Local Similarity 86.2%; Pred. No. 6.2e-42;
Matches 94; Conservative 9; Mismatches 3; Indels 3; Gaps 1;

Qy 1 SQIPASEQETLVPRKPLLLKLSVGAQKDTYTMKEVLYLGGYIMTKRLYDEKQOHIHVH 60
|||||
Db 17 SQIPASEQETLVPRKPLLLKLSVGAQNDVTYMKELIIFIGYIMTKRLYDEKQOHIYV 76
|||||

Qy 61 CSNDLLGLDFGVPSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 109
|||||
Db 77 CSNDLLGLDFGVPSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 122
|||||

RESULT 3
S1955
MDM2-like p53-binding protein MDMX - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
C:Accession: S1955
R:Shvarits, A.; Steegenga, W.T.; Riteco, N.; van Laar, T.; Dekker, P.; Bazuine, M.; van H
EMBO J. 15, 5349-5357, 1996
A:Title: MDMX: a novel p53-binding protein with some functional properties of MDM2.
A:Reference number: S1955; MUID:97050840; PMID:8895579
A:Accession: S1955
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-489 <SHV>
A:Cross-references: UNIPROT:Q35618; EMBL:AF007110; NID:g2253388; PIDN:AAB62927.1; PID:g2
C:Genetics:
A:Gene: MDMX
C:Function:
A:Description: inhibits transcription activation function of tumour suppressor protein p
C:Superfamily: human p53-binding protein mdm2

Query Match 49.5%; Score 274.5; DB 2; Length 489;
Best Local Similarity 52.4%; Pred. No. 2.5e-20;
Matches 55; Conservative 18; Mismatches 21; Indels 11; Gaps 1;

Qy 5 ASEQETLVPRKPLLLKLSVGAQKDTYTMKEVLYLGGYIMTKRLYDEKQOHIHVCSND 64
|||||
Db 20 SSEQISQVRPKQLLLKILFAAGAQGEVFTMKVHLYGLYIMVKOLYDQEQHMYVCGD 79
|||||

Qy 65 LLGLDFGVPSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 109
|||||
Db 80 LLGLDGLGCQSFVKDPSFLYDMLRNLV-----TSASNN 113
|||||

RESULT 4
SXBPT4
```

```
NAD+-protein ADP-ribosyltransferase (EC 2.4.2.-) precursor - phase T4
C:Species: phase T4
A:Note: host Escherichia coli
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C:Accession: JU0096
R:Hilse, D.; Koch, T.; Rueger, W.
Nucleic Acids Res. 17, 6731, 1989
A:Title: Nucleotide sequence of the alt gene of bacteriophage T4.
A:Reference number: JU0096; MUID:89386005; PMID:2506526
A:Accession: JU0096
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-685 <Hil>
A:Cross-references: UNIPROT:P12726
C:Comment: This enzyme catalyzes the ADP-ribosylation of one of the two alpha-subunits c
C:Genetics:
A:Gene: alt
C:Superfamily: phase T4 NAD-protein ADP-ribosyltransferase
C:Keywords: glycosyltransferase; pentosyltransferase
C:Keywords: NAD-protein ADP-ribosyltransferase #status predicted <MAT>
F:7-685/Product: NAD-protein ADP-ribosyltransferase #status predicted <MAT>

Query Match 15.0%; Score 83; DB 1; Length 685;
Best Local Similarity 29.0%; Pred. No. 1.5;
Matches 29; Conservative 22; Mismatches 35; Indels 14; Gaps 6;

Qy 18 LLKLLKS--VGAQKDTYTMKEVLYL--GOYIMTKRL--YDEKQOHI-VHCSNDLLGLD 69
|||||
Db 111 MLRLKSKTAGAQARQIQVIADRLRSRGGRYVLKELWDYDKKYAYILIRKKNVSLDI 170
|||||

Qy 70 FGVPFSFVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 109
|||||
Db 171 PGVPEISTELFTKVESKV--GDVVINK---DTGAQVTKN 204
|||||

RESULT 5
S31630
NAD+-protein ADP-ribosyltransferase (EC 2.4.2.-) precursor - phase T2
C:Species: phase T2
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S31630
R:Koch, T.; Rueger, W.
A:Description: The ADP-ribosyltransferase of bacteriophages T2, T4 and T6: Sequencing of
A:Reference number: S31630
A:Accession: S31630
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-698 <KOC>
A:Cross-references: UNIPROT:Q38424; EMBL:X69893; NID:g15187; PIDN:CAA49517.1; PID:g15188
C:Superfamily: phase T4 NAD-protein ADP-ribosyltransferase
C:Keywords: glycosyltransferase; NAD; pentosyltransferase

Query Match 15.0%; Score 83; DB 1; Length 698;
Best Local Similarity 29.0%; Pred. No. 1.6;
Matches 29; Conservative 22; Mismatches 35; Indels 14; Gaps 6;

Qy 18 LLKLLKS--VGAQKDTYTMKEVLYL--GOYIMTKRL--YDEKQOHI-VHCSNDLLGLD 69
|||||
Db 112 MLRLKSKTAGAQARQIQVIADRLRSRGGRYVLKELWDYDKKYAYILIRKKNVSLDI 171
|||||

Qy 70 FGVPFSFVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 109
|||||
Db 172 PGVPEISTELFTKVESKV--GDVVINK---DTGAQVTKN 205
|||||

RESULT 6
S31714
NAD+-protein ADP-ribosyltransferase (EC 2.4.2.-) precursor - phase T6
C:Species: phase T6
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S31714
R:Koch, T.; Rueger, W.
submitted to the EMBL Data Library, December 1992
```

[illegible]

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Qy      1  SQIPASEQEFTLVRPKPLLLKLLKSVAQKDQTYTMKEVLYYLGYOYIMTKR---LYDEKQQH 57
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db     768 NEIKNQEQEGLRELEELFIIYQNLIKDKISYQMRETT-----IKRKNDADFVDERGEI 821
       ||::||::||::||::||::||::||::||::||::||::||::||::||::||:

Qy     58 IVHCSDNLLGDLFGVPSPFSVKHRKIYTMIRNLAVVVNQESSDS 102
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db    822 REFLDGSLGADKYIEKNSSVRE-----KCLYENFMQVDSEIEKDT 861
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||:

RESULT 10
D85069
hypothetical protein At4g05520 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: D85069
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The C
Nature 402, 769-777, 1999
A>Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thalian
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: D85069
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-514 <STO>
A:Cross-references: UNIPROT:Q9S9W1; GB:N_001268; NID:g7267312; PIDN:CAB81094.1
C:Genetics:
A:Gene: At4g05520
A:Map position: 4

Query Match          12.9%; Score 71.5; DB 2; Length 514;
Best Local Similarity 29.7%; Pred.No.16;
Matches 27; Conservative 13; Mismatches 26; Indels 25; Gaps 4;
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Query Match      12.5%; Score 69.5; DB 2; Length 709;
Best Local Similarity 23.4%; Pred. No. 38;
Matches 22; Conservative 18; Mismatches 45; Indels 9; Gaps 2
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Search completed: January 27, 2005, 18:15:11  
Job time : 20.8 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:51:46 ; Search time 84.6 Seconds  
(without alignments)  
741.322 Million cell updates/sec

Title: US-10-822-254-10  
Perfect score: 555  
Sequence: 1 SQIPASEQETLVRPKPLLLK.....NLVVNQESSDSGTSVSEN 109

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 02.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	545	98.2	166	Q8NDW2	Q8ndw2 homo sapien
2	545	98.2	195	Q96DS4	Q96ds4 homo sapien
3	545	98.2	243	Q8TE47	Q8te47 homo sapien
4	545	98.2	491	1 MD2 HUMAN	Q00987 homo sapien
5	545	98.2	491	2 AAP35922	Aap35922 homo sapi
6	545	98.2	491	2 AAH67077	Aah67077 homo sapi
7	533	96.0	487	1 MD2 CANFA	P56950 canis famil
8	533	96.0	487	2 Q9GMZ6	Q9gmz6 canis famil
9	533	96.0	491	1 MD2 HORSE	P56951 equus cabal
10	530	95.5	491	2 Q7YRZ8	Q7yrz8 felis silve
11	495	89.2	436	2 Q8WYJ2	Q8wyj2 homo sapien
12	485.5	87.5	489	1 MD2 MOUSE	P23804 mus musculu
13	485.5	87.5	489	2 Q91XK7	Q91xk7 m mus muscu
14	468	84.3	118	2 Q8WYJ3	Q8wyj3 homo sapien
15	463.5	83.5	466	1 MD2 MESAU	Q60524 mesocricetu
16	418	75.3	325	2 Q9PVL2	Q9pvl2 gallus gall
17	399	71.9	173	2 Q8TE45	Q8te46 homo sapien
18	368	66.3	473	1 MD2 XENLA	P56273 xenopus lae
19	368	66.3	473	2 Q6GMB5	Q6gmb5 xenopus lae
20	367	66.1	482	2 Q6P3Q9	Q6p3q9 xenopus tro
21	367	66.1	482	2 AAH63898	Aah63898 xenopus t
22	331	59.6	105	2 Q8NDW0	Q8ndw0 homo sapien
23	315	56.8	426	2 Q9GK41	Q9gk41 canis famil
24	295.5	53.2	445	1 MD2 BRARE	O42354 brachydanio
25	295.5	53.2	445	2 AAM00198	Aam00198 brachydan
26	280.5	50.5	446	2 Q8WYJ1	Q8wyj1 homo sapien
27	277	49.9	491	2 Q7ZUW7	Q7zuw7 brachydanio
28	275	49.5	475	2 Q7ZYI3	Q7zyi3 xenopus lae
29	274.5	49.5	489	1 MD4 MOUSE	O35618 mus musculu
30	271.5	48.9	489	2 Q9CYG1	Q9cyg1 m mus muscu
31	265	47.7	490	2 Q99L86	Q99l86 mus musculu

32	263.5	47.5	134	2 Q6PHL8	Q6phl8 xenopus lae
33	263.5	47.5	134	2 AAH56503	Aah56503 xenopus l
34	249	44.9	153	2 Q6MZR7	Q6mzr7 homo sapien
35	249	44.9	153	2 CAE45961	Caeh45961 homo sapi
36	249	44.9	490	2 AAH67299	Aah67299 homo sapi
37	247	44.5	490	1 MD4 HUMAN	O15151 homo sapien
38	220	39.6	69	2 Q86WA4	Q86wa4 homo sapien
39	213	38.4	66	2 Q96DS3	Q96ds3 homo sapien
40	210	37.8	70	2 Q86WA3	Q86wa3 homo sapien
41	196	35.3	95	2 Q96DS1	Q96ds1 homo sapien
42	179.5	32.3	70	2 Q8NDW1	Q8ndw1 homo sapien
43	177	31.9	159	2 Q96DS0	Q96ds0 homo sapien
44	176	31.7	60	2 Q96DS5	Q96ds5 homo sapien
45	176	31.7	130	2 Q9H4C3	Q9h4c3 homo sapien

#### ALIGNMENTS

##### RESULT 1

Q8NDW2 PRELIMINARY; PRT; 166 AA.  
AC Q8NDW2;  
DT 01-OCT-2002 (TRENBLrel. 22, Created)  
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
DE P53-binding protein.  
GN Name=MDM2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bartel F., Pinkert D., Kappeler M., Bache M., Schmidt H., Taubert H.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ491698; CAD36959.1; -.  
DR HSSP; Q9UMT8; 1YCR.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR InterPro; IPR001984; MDM2.  
DR InterPro; IPR003121; SWIB\_MDM2.  
DR Pfam; PF02201; SWIB; 1  
SQ SEQUENCE 166 AA; 18900 MW; FA6B5BA18E85040D CRC64;

Query Match 98.2%; Score 545; DB 2; Length 166;  
Best Local Similarity 98.2%; Pred. No. 4.5e-50;  
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTKVELVYYLQYIMTKRLYDEKQOHIVH 60

Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTKVELVYYLQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVSPSVKHEHKIYTMIVRNVLVVNQESSDSGTSVSEN 109

Db 77 CSNDLLGDLFGVSPSVKHEHKIYTMIVRNVLVVNQESSDSGTSVSEN 125

##### RESULT 2

Q96DS4 PRELIMINARY; PRT; 195 AA.  
AC Q96DS4;  
DT 01-DEC-2001 (TRENBLrel. 19, Created)  
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
DE MDM2 variant FB26.  
GN Name=MDM2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Rhabdomyosarcoma tumor;

RA Bartel F., Taylor A.C., Taubert H., Harris L.C.;  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF385323; AALJ3243.1; --  
 DR HSP; Q9UMT8; 1YCR.

DR GO; GO:0005634; C:nucleus; IEA.

DR InterPro; IPR010984; MDM2.

DR Pfam; PF02201; SWIB; 1.

SQ SEQUENCE 195 AA; 22161 MW; 4987AE567DB12D5D CRC64;

Query Match 98.2%; Score 545; DB 2; Length 195;

Best Local Similarity 98.2%; Pred. No. 5.4e-50;

Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVH 60

Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGLDFGVPSFSVKEHRKIYTMVYRNLVVNVNQSSDSGTSVSEN 109

Db 77 CSNDLLGLDFGVPSFSVKEHRKIYTMVYRNLVVNVNQSSDSGTSVSEN 125

# RESULT 3

Q8TE47

ID Q8TE47 PRELIMINARY; PRT; 243 AA.

AC Q8TE47;

DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE MDM2 isoform KB9 protein.

GN Name=MDM2 isoform KB9;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Lymphocytes;

RA Bartel F., Pinkert D., Kappler M., Bache M., Schmidt H., Taubert H.;

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ430612; CAD23251.1; --

DR HSP; Q9UMT8; 1YCR.

DR GO; GO:0005634; C:nucleus; IEA.

DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.

DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.

DR GO; GO:0008270; F:zinc ion binding; IEA.

DR GO; GO:0016567; P:protein ubiquitination; IEA.

DR InterPro; IPR010984; MDM2.

DR InterPro; IPR003121; SWIB\_MDM2.

DR Pfam; PF02201; SWIB; 1.

DR SMART; SM00184; RING; 1.

DR PROSITE; PS50089; ZF\_RING\_2; 1.

SQ SEQUENCE 243 AA; 27317 MW; 9EB5D0142CF185A2 CRC64;

Query Match

Best Local Similarity 98.2%; Score 545; DB 2; Length 243;

Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVH 60

Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGLDFGVPSFSVKEHRKIYTMVYRNLVVNVNQSSDSGTSVSEN 109

Db 77 CSNDLLGLDFGVPSFSVKEHRKIYTMVYRNLVVNVNQSSDSGTSVSEN 125

# RESULT 4

MDM2 HUMAN

ID MDM2 HUMAN STANDARD; Q13226; Q13297; Q13298; Q13299; Q13300; Q13301; Q9UGI3;

AC Q00987; Q13226; Q13297; Q13298; Q13299; Q13300; Q13301; Q9UGI3;

AC

DT

DT

DT

DE

DE

GN

OS

OC

OC

OX

RN

RP

RX

RA

RT

RT

RL

RN

RP

RC

RA

RT

RT

RL

RN

RP

RX

RA

RT

RT

RL

RN

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RC

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RC

RA

RT

RT

RL

RN

RP

RC

RA

RT

RT

RL

RN

RP

RC

RA

RT

RT

RL

RN

Q9UMT8;

01-APR-1993 (Rel. 25, Created)

01-APR-1993 (Rel. 25, Last sequence update)

01-OCT-2004 (Rel. 45, Last annotation update)

Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Hdm2).

Name=MDM2;

Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI\_TaxID=9606;

[1]

SEQUENCE FROM N.A. (ISOFORM MDM2).

MEDLINE=92310576; PubMed=1614537;

Oliner J.D., Kinzler K.W., Meltzer P.S., George D.L., Vogelstein B.;

"Amplification of a gene encoding a p53-associated protein in human

sarcomas";

Nature 358:80-83 (1992).

[2]

SEQUENCE FROM N.A. (ISOFORMS MDM2-A; -B; -C; -D AND -E).

TISSUE=Ovarian carcinoma;

MEDLINE=96313107; PubMed=8705862;

Sigalas I., Calvert A.H., Anderson J.J., Neal D.E., Lunec J.;

"Alternatively spliced mdm2 transcripts with loss of p53 binding

domain sequences: transforming ability and frequent detection in human

cancer.";

Nat. Med. 2:912-917 (1996).

[3]

SEQUENCE FROM N.A. (ISOFORM MDM2-ALPHA).

MEDLINE=20065171; PubMed=10597303;

Veidhoen N., Metcalfe S., Milner J.;

"A novel exon within the mdm2 gene modulates translation initiation in

vitro and disrupts the p53-binding domain of mdm2 protein.";

Oncogene 18:7026-7033 (1999).

[4]

SEQUENCE FROM N.A. (ISOFORM MDM2).

Rieder M.J., Livingston R.J., Braun A.C., Montoya M.A., Chung M.-W.,

Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,

Shackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;

"NIHES-SNPs, environmental genome project, NIHES ES15478, Department

of Genome Sciences, Seattle, WA (URL: http://segs.washington.edu).";

Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

[5]

SEQUENCE FROM N.A. (ISOFORM MDM2).

TISSUE=Muscle;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

[6]

SEQUENCE OF 6-491 FROM N.A. (ISOFORM MDM2-A1).

Liang H., Atkins H., Abdel-Fattah R., Saeed R., Lunec J.;

"Genomic organisation of the human MDM2 oncogene and relationship to

its alternatively spliced mRNA's";

Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

[7]

RP SEQUENCE OF 1-24 FROM N.A.  
RX MEDLINE=95380270; PubMed=7651818;  
RA Zauberman A., Flusberg D., Haupt Y., Barak Y., Oren M.;  
RT "A functional p53-responsive intronic promoter is contained within the  
RL human mdm2 gene.";  
RN Nucleic Acids Res. 23:2584-2592(1995).  
RP SEQUENCE OF 1-9 FROM N.A.  
RX MEDLINE=97413643; PubMed=9270029;  
RA Landers J.B., Cassel S.L., George D.L.;  
RT "Translational enhancement of mdm2 oncogene expression in human tumor  
RL cells containing a stabilized wild-type p53 protein.";  
RN Cancer Res. 57:3562-3568(1997).  
RP SEQUENCE OF 301-481 FROM N.A.  
RX MEDLINE=20542019; PubMed=11087894;  
RA Taubert H., Kappler M., Meyer A., Bartel F., Schlott T.,  
RL Lautenschlaeger C., Bache M., Schmidt H., Wuerl P.;  
RT "A MboII polymorphism in exon 11 of the human MDM2 gene occurring in  
RL normal blood donors and in soft tissue sarcoma patients: an indication  
RL for an increased cancer susceptibility?";  
RN Mutat. Res. 456:39-44(2000).  
RP MUTAGENESIS OF CYS-464.  
RX MEDLINE=98111004; PubMed=9450543;  
RA Honda R., Tanaka H., Yasuda H.;  
RT "Oncoprotein MDM2 is a ubiquitin ligase E3 for tumor suppressor p53.";  
RL FEBS Lett. 420:25-27(1997).  
RP MUTAGENESIS OF CYS-449.  
RX MEDLINE=20190101; PubMed=10723139;  
RA Honda R., Yasuda H.;  
RT "Activity of MDM2, a ubiquitin ligase, toward p53 or itself is  
RL dependent on the RING finger domain of the ligase.";  
RN Oncogene 19:1473-1476(2000).  
RP MUTAGENESIS.  
RX MEDLINE=20187618; PubMed=10722742;  
RA Fang S., Jensen J.P., Ludwig R.L., Vousden K.H., Weisman A.M.;  
RT "Mdm2 is a RING finger-dependent ubiquitin protein ligase for itself  
RL and p53.";  
RL J. Biol. Chem. 275:8945-8951(2000).  
RP [13]  
RX MUTAGENESIS OF CYS-441 AND CYS-478.  
RX MEDLINE=20076498; PubMed=10608892;  
RA Sharp D.A., Kratowicz S.A., Sank M.J., George D.L.;  
RT "Stabilization of the MDM2 oncoprotein by interaction with the  
RL structurally related MDMX protein.";  
RL J. Biol. Chem. 274:38189-38196(1999).  
RP [14]  
RX NUCLEOLAR LOCALIZATION SIGNAL.  
RX MEDLINE=20173879; PubMed=10707090;  
RA Lohrum M.A.E., Ashcroft M., Kubbutat M.H.G., Vousden K.H.;  
RT "Identification of a cryptic nucleolar-localization signal in MDM2.";  
RN Nat. Cell Biol. 2:179-181(2000).  
RP [15]  
RX PHOSPHORYLATION BY ATM.  
RX MEDLINE=20079591; PubMed=10611322;  
RA Khosravi R., Maya R., Gottlieb T., Oren M., Shiloh Y., Shkedy D.;  
RT "Rapid ATM-dependent phosphorylation of MDM2 precedes p53 accumulation  
RL in response to DNA damage.";  
RL Proc. Natl. Acad. Sci. U.S.A. 96:14973-14977(1999).  
RP [16]  
RX X-RAY CRYSTALLOGRAPHY (2.6 ÅNGSTROMS) OF 25-109 IN COMPLEX WITH P53.  
RX MEDLINE=97081050; PubMed=8875929;  
RA Kussie P.H., Gorina S., Marechal V., Elenbaas B., Moreau J.,  
RA Levine A.J., Pavletich N.P.;  
RT "Structure of the MDM2 oncoprotein bound to the p53 tumor suppressor  
RL transactivation domain.";  
RL Science 274:948-953(1996).  
CC -! FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and  
CC apoptosis by binding its transcriptional activation domain.  
CC Functions as a ubiquitin ligase E3, in the presence of E1 and E2,

CC toward p53 and itself. Permits the nuclear export of p53 and  
CC targets it for proteasome-mediated proteolysis.  
CC -! COFACTOR: Zinc is required for ubiquitin ligase E3 activity.  
CC -! SUBUNIT: Binds p53, p73, ARF(P14), ribosomal protein L5 and  
CC specifically to RNA. Can interact also with retinoblastoma protein  
CC (RB), E1A-associated protein EP300 and the E2F1 transcription  
CC factor.  
CC -! SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed  
CC predominantly in the nucleoplasm. Interaction with ARF(P14)  
CC results in the localization of both proteins to the nucleolus. The  
CC nucleolar localization signals in both ARF(P14) and MDM2 may be  
CC necessary to allow efficient nucleolar localization of both  
CC proteins.  
CC -! ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=8;  
CC Name=Mdm2;  
CC IsoId=Q00987-1; Sequence=Displayed;  
CC Name=Mdm2-A;  
CC IsoId=Q00987-2; Sequence=VSP\_003208;  
CC Name=Mdm2-A1;  
CC IsoId=Q00987-3; Sequence=VSP\_003208, VSP\_003214;  
CC Name=Mdm2-B;  
CC IsoId=Q00987-4; Sequence=VSP\_003209;  
CC Name=Mdm2-C;  
CC IsoId=Q00987-5; Sequence=VSP\_003211;  
CC Name=Mdm2-D;  
CC IsoId=Q00987-6; Sequence=VSP\_003210;  
CC Name=Mdm2-E;  
CC IsoId=Q00987-7; Sequence=VSP\_003212, VSP\_003213;  
CC Name=Mdm2-alpha;  
CC IsoId=Q00987-8; Sequence=VSP\_003207;  
CC -! TISSUE SPECIFICITY: Ubiquitous. Isoforms MDM2-A, -B, -C, -D and -E  
CC are observed in a range of human cancers but absent in normal  
CC tissues.  
CC -! INDUCTION: By DNA damage.  
CC -! DOMAIN: Region I is sufficient for binding p53 and inhibiting its  
CC G1 arrest and apoptosis functions. It also binds p73 and E2F1.  
CC Region II contains most of a central acidic region required for  
CC interaction with ribosomal protein L5 and a putative C4-type zinc  
CC finger. The RING finger domain which coordinates two molecules of  
CC zinc interacts specifically with RNA whether or not zinc is  
CC present and mediates the hetero-oligomerization with MDM4. It is  
CC also essential for its ubiquitin ligase E3 activity toward p53 and  
CC itself.  
CC -! PTM: Phosphorylated in response to ionizing radiation in an ATM-  
CC dependent manner.  
CC -! DISEASE: Seems to be amplified in certain tumors (including soft  
CC tissue sarcomas, osteosarcomas and gliomas). A higher frequency of  
CC splice variants lacking p53 binding domain sequences was found in  
CC late-stage and high-grade ovarian and bladder carcinomas. Four of  
CC the splice variants show loss of p53 binding.  
CC -! MISCELLANEOUS: MDM2 RING finger mutations that failed to  
CC Query Match 98.2%; Score 545; DB 1; Length 491;  
CC Best Local Similarity 98.2%; Pred. No. 1.6e-49;  
CC Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SQIPASEQETLVPRPKLLKLLKSVGAQKQYTVKVELVYLGYITMKRLYDEKQOHLVH 60  
Db 17 SQIPASEQETLVPRPKLLKLLKSVGAQKQYTVKVELVYLGYITMKRLYDEKQOHLVH 76  
Qy 61 CSNDLLGDLFGVPSFVKHKKIYTMVYRNVLVNVNQESSDSGTSVSEN 109  
Db 77 CSNDLLGDLFGVPSFVKHKKIYTMVYRNVLVNVNQESSDSGTSVSEN 125  
RESULT 5  
AAP35922 PRELIMINARY; PRT; 491 AA.  
ID AAP35922  
AC AAP35922  
DT 02-MAR-2004 (TremBLrel. 27, Created)  
DT 02-MAR-2004 (TremBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TremBLrel. 27, Last annotation update)

DE Mdm2, transformed 3T3 cell double minute 2, p53 binding protein  
DE (Mouse).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kaline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,  
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,  
RA Phelan M., Farmer A.;  
RA "Cloning of human full-length cDNAs in BD Creator(TM) System Donor  
RT vector";  
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BT007258; AAF35922.1; F37CE163876BC983 CRC64;  
SQ SEQUENCE 491 AA; 55232 MW; F37CE163876BC983 CRC64;  
Query Match 98.2%; Score 545; DB 2; Length 491;  
Best Local Similarity 98.2%; Pred. No. 1.6e-49;  
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVH 60  
DB 17 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVY 76  
QY 61 CSNDLLGDLFGVPSFVKHKKIYTMIRNVLVNVNQSSDSGTSVSEN 109  
DB 77 CSNDLLGDLFGVPSFVKHKKIYTMIRNVLVNVNQSSDSGTSVSEN 125  
RESULT 6  
AAH67077  
ID AAH67077 PRELIMINARY; PRT; 491 AA.  
AC AAH67077;  
DT 14-APR-2004 (TrEMBLrel. 27, Created)  
DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 14-APR-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Muscle;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Hellon E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalek A., Smaluk D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Muscle;  
RA Strausberg R.;  
RA Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC067077; AAH67077.1;  
KW Hypothetical protein.

SQ SEQUENCE 491 AA; 55232 MW; F37CE163876BC983 CRC64;  
Query Match 98.2%; Score 545; DB 2; Length 491;  
Best Local Similarity 98.2%; Pred. No. 1.6e-49;  
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVH 60  
DB 17 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVY 76  
QY 61 CSNDLLGDLFGVPSFVKHKKIYTMIRNVLVNVNQSSDSGTSVSEN 109  
DB 77 CSNDLLGDLFGVPSFVKHKKIYTMIRNVLVNVNQSSDSGTSVSEN 125  
RESULT 7  
MDM2 CANFA  
ID MDM2 CANFA STANDARD; PRT; 487 AA.  
AC P56950; Q95KNS;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein  
DE Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Cdm2).  
GN Name=MDM2;  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE OF 1-484 FROM N.A.  
RX MEDLINE=20218866; PubMed=10754200;  
RA Nasir L., Burr P.D., McFarlane S.T., Gault E., Thompson H.,  
RA Argyle D.J.;  
RT "Cloning, sequence analysis and expression of the cDNAs encoding the  
RT canine and equine homologues of the mouse double minute 2 (mdm2)  
RT proto-oncogene.";  
RL Cancer Lett. 152:9-13 (2000).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS MDM2 AND MDM2-ALPHA).  
RX MEDLINE=20065171; PubMed=10597303;  
RA Verdoorn N., Metcalfe S., Milner J.;  
RT "A novel exon within the mdm2 gene modulates translation initiation in  
RT vitro and disrupts the p53-binding domain of mdm2 protein.";  
RL Oncogene 18:7026-7033 (1999).  
CC -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and  
CC apoptosis by binding its transcriptional activation domain.  
CC Functions as a ubiquitin ligase E3, in the presence of E1 and E2,  
CC toward p53 and itself. Permits the nuclear export of p53 and  
CC targets it for proteasome-mediated proteolysis (By similarity).  
CC -!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity (By  
CC similarity).  
CC -!- SUBUNIT: Binds p53, p73, ARF (P14), ribosomal protein L5 and  
CC specifically to RNA. Can interact also with retinoblastoma protein  
CC (RB), E1A-associated protein E1300 and the E2F1 transcription  
CC factor (By similarity).  
CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed  
CC predominantly in the nucleoplasm (By similarity).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=Mdm2;  
CC IsoId=P56950-1; Sequence=Displayed;  
CC Name=Mdm2-alpha;  
CC IsoId=P56950-2; Sequence=VSP 003206;  
CC -!- TISSUE SPECIFICITY: Isoform Mdm2-alpha is present in lymphoid and  
CC testicular tissues.  
CC -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its  
CC G1 arrest and apoptosis functions. It also binds p73 and E2F1.  
CC Region II contains most of a central acidic region required for  
CC interaction with ribosomal protein L5 and a putative C4-type zinc  
CC finger. The RING finger domain which coordinates two molecules of  
CC zinc interacts specifically with RNA whether or not zinc is  
CC present and mediates the hetero-oligomerization with MDM4. It is

OX	NCBI_TaxID=9615;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Liver;
RA	TSotoguchi A., Tautjimoto H.;
RL	Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AB031276; BAB11975.1; -.
DR	HSP; Q9UNT8; IYCR.
DR	GO; GO:0005730; C:nucleolus; ISS.
DR	GO; GO:0005654; C:nucleoplasm; ISS.
DR	GO; GO:0017163; F:negative regulator of basal transcription a. . .; ISS.
DR	GO; GO:0005125; F:protein binding; ISS.
DR	GO; GO:0000122; F:negative regulation of transcription from P. . .; ISS.
DR	InterPro; IPR010984; MDM2.
DR	InterPro; IPR003121; SWIB MDM2.
DR	InterPro; IPR001876; Znf_RanGDP.
DR	InterPro; IPR001841; Znf_Ring.
DR	Pfam; PF02201; SWIB; 1.
DR	Pfam; PF00641; Zf-RanBP; 1.
DR	SMART; SM00184; RING; 1.
DR	PROSITE; PS01358; ZF_RANBP2_1; 1.
DR	PROSITE; PS01099; ZF_RANBP2_2; 1.
DR	PROSITE; PS00089; ZF_RING_2; 1.
SQ	SEQUENCE 487 AA; 54724 MW; 34FC5CC6A18D7744 CRC64;
	Query Match 96.0%; Score 533; DB 2; Length 487;
	Best Local Similarity 95.4%; Pred. No. 3e-48;
	Matches 104; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy	1 SQIPASEQETLVRPKPLLKLLKLSVGAQKDTYTMKEVLYLGQVIMTKRLYDEKQIHV 60
Db	17 SQIPASEQETLVRPKPLLKLLKLSVGAQKDTYTMKEVIFYLGQVIMTKRLYDEKQIHV 76
Qy	61 CSNDLLGDLFGVPSFVKHKRTYTMIRNLVVVNQOESSDGTGSVEN 109
Db	77 CSNDLLGDLFGVPSFVKHKRTYTMIRNLVVVNQOHPSDGTGSVEN 125
RESULT 9	
MDM2_HORSE	
ID	MDM2_HORSE STANDARD; PRT; 491 AA.
AC	P56951;
DT	30-MAY-2000 (Rel. 39, Created)
DT	30-MAY-2000 (Rel. 39, Last sequence update)
DE	05-JUL-2004 (Rel. 44, Last annotation update)
DE	Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein
DE	Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Edm2).
GN	Names=MDM2;
OS	Equus caballus (Horse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX	NCBI_TaxID=9796;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	MEDLINE=202118866; PubMed=10754200;
RA	Nasir L., Burr P.D., McFarlane S.T., Gault E., Thompson H.,
RA	Argyle D.J.;
RT	"Cloning, sequence analysis and expression of the cDNAs encoding the
RT	canine and equine homologues of the mouse double minute 2 (mdm2)
RT	proto-oncogene.";
RL	Cancer Lett. 152:9-13(2000).
CC	-1- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and
CC	apoptosis by binding its transcriptional activation domain.
CC	Functions as a ubiquitin ligase E3, in the presence of E1 and E2,
CC	toward p53 and itself. Permits the nuclear export of p53 and
CC	targets it for proteasome-mediated proteolysis (By similarity).
CC	-1- COFACTOR: Zinc is required for ubiquitin ligase E3 activity (By
CC	similarity).
CC	-1- SUBUNIT: Binds p53, p73, ARF (P14), ribosomal protein L5 and
CC	specifically to RNA. Can interact also with retinoblastoma protein
CC	(RB), E1A-associated protein E3P00 and the E2F1 transcription
CC	factor (By similarity).
CC	-1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed

predominantly in the nucleoplasm (By similarity).  
 -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its G1 arrest and apoptosis functions. It also binds p73 and E2F1.  
 Region II contains most of a central acidic region required for interaction with ribosomal protein L5 and a putative C4-type zinc finger. The RING finger domain which coordinates two molecules of zinc interacts specifically with RNA whether or not zinc is present and mediates the hetero-oligomerization with MDM4. It is also essential for its ubiquitin ligase E3 activity toward p53 and itself (By similarity).  
 -!- SIMILARITY: Belongs to the MDM2 / MDM4 family.  
 -!- SIMILARITY: Contains 1 RANBP2-type zinc finger.  
 -!- SIMILARITY: Contains 1 RING-type zinc finger.  
 -!- SIMILARITY: Contains 1 SWIB domain.  
 -----  
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EMBL; AF121140; AAF28866.1; -.  
 DR HSSP; Q9UMT8; 1YCR.  
 DR InterPro; IPR010984; MDM2.  
 DR InterPro; IPR003121; SWIB.  
 DR InterPro; IPR001876; Znf\_RanGDP.  
 DR InterPro; IPR001841; Znf\_Ring.  
 DR Pfam; PF02201; SWIB; 1.  
 DR Pfam; PF00641; zf-RanBP; 1.  
 DR SMART; SM00184; RING; 1.  
 DR PROSITE; PS01358; ZF\_RANBP2\_1; 1.  
 DR PROSITE; PS01358; ZF\_RANBP2\_2; 1.  
 DR PROSITE; PS00518; ZF\_RING\_1; FALSE\_NEG.  
 DR PROSITE; PS00089; ZF\_RING\_2; 1.  
 DR Ligase; Metal-binding; Nuclear protein; Ubl conjugation pathway; Zinc; Zinc-finger.  
 FT DOMAIN 27 107 SWIB.  
 FT DOMAIN 179 185 Nuclear localization signal (Potential).  
 FT DOMAIN 190 202 Nuclear export signal.  
 FT DOMAIN 210 304 Arkf-binding.  
 FT DOMAIN 210 215 Poly-Ser.  
 FT DOMAIN 242 331 Region II.  
 FT DOMAIN 243 301 Asp/Glu-rich (acidic).  
 FT ZN\_FING 299 328 RANBP2-type.  
 FT ZN\_FING 438 479 RING-type.  
 FT DOMAIN 466 473 Nuclear localization signal (Potential).  
 FT SEQUENCE 491 AA; 55279 MW; 641E033D5C1DEC39 CRC64;

Query Match 96.0%; Score 533; DB 1; Length 491;  
 Best Local Similarity 95.4%; Pred. No. 3e-48; Mismatches 4; Indels 0; Gaps 0;  
 Matches 104; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTWKVELVYLQYIMTKRLYDEKQOHIVH 60  
 Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTWKVELVYLQYIMTKRLYDEKQOHIVY 76  
 QY 61 CSNDLLGDLFGVPSFVKHEKRIYTIYRNLVVNVNQSSDSGTSVSEN 109  
 Db 77 CSNDLLGDLFGVPSFVKHEKRIYTIYRNLVVNVNQSSDSGTSVSEN 125

RESULT 10  
 QYRZ8  
 ID Q7YRZ8 PRELIMINARY; PRT; 491 AA.  
 AC Q7YRZ8;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Double minute 2 protein MDM2.  
 GN Name=mdm2;

OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 OX NCBI\_TaxID=9685;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RL Miki R., Okuda M., Ma Z., Inokuma H., Onishi T.;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB099709; BAC78209.1; -.  
 DR GO; GO:0005730; C:nucleolus; ISS.  
 DR GO; GO:0005654; C:nucleoplasm; ISS.  
 DR GO; GO:0017163; F:negative regulator of basal transcription a...; ISS.  
 DR GO; GO:0005515; F:protein binding; ISS.  
 DR GO; GO:0000122; P:negative regulation of transcription from P...; ISS.  
 DR InterPro; IPR003121; SWIB\_MDM2.  
 DR InterPro; IPR001876; Znf\_RanGDP.  
 DR InterPro; IPR001841; Znf\_Ring.  
 DR Pfam; PF02201; SWIB; 1.  
 DR Pfam; PF00641; zf-RanBP; 1.  
 DR SMART; SM00184; RING; 1.  
 DR PROSITE; PS01358; ZF\_RANBP2\_1; 1.  
 DR PROSITE; PS01358; ZF\_RANBP2\_2; 1.  
 DR PROSITE; PS00089; ZF\_RING\_2; 1.  
 DR PROSITE; PS00089; ZF\_RING\_2; 1.  
 DR SEQUENCE 491 AA; 55433 MW; D93E25D638E8934 CRC64;  
 Query Match 95.5%; Score 530; DB 2; Length 491;  
 Best Local Similarity 94.5%; Pred. No. 6.3e-48;  
 Matches 103; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTWKVELVYLQYIMTKRLYDEKQOHIVH 60  
 Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTWKVELVYLQYIMTKRLYDEKQOHIVY 76  
 QY 61 CSNDLLGDLFGVPSFVKHEKRIYTIYRNLVVNVNQSSDSGTSVSEN 109  
 Db 77 CSNDLLGDLFGVPSFVKHEKRIYTIYRNLVVNVNQSSDSGTSVSEN 125  
 RESULT 11  
 Q8WYJ2  
 ID Q8WYJ2 PRELIMINARY; PRT; 436 AA.  
 AC Q8WYJ2;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE MDM2 protein.  
 GN Name=MDM2;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RL MEDLINE=21248713; PubMed=11351297;  
 RA Tamborini E., Della Torre G., Lavarino C., Azzarelli A.,  
 RA Carpinelli P., Pierotti M.A., Pilotti S.;  
 RT "Analysis of the molecular species generated by MDM2 gene  
 RT amplification in liposarcomas."  
 RL Int. J. Cancer 92:790-796(2001).  
 DR EMBL; AF092844; AAL40179.1; -.  
 DR HSSP; Q9UMT8; 1YCR.  
 DR GO; GO:0005730; C:nucleolus; ISS.  
 DR GO; GO:0005654; C:nucleoplasm; ISS.  
 DR GO; GO:0017163; F:negative regulator of basal transcription a...; ISS.  
 DR GO; GO:0005515; F:protein binding; ISS.  
 DR GO; GO:0000122; P:negative regulation of transcription from P...; ISS.  
 DR InterPro; IPR010984; MDM2.  
 DR InterPro; IPR003121; SWIB\_MDM2.  
 DR InterPro; IPR001876; Znf\_RanGDP.  
 DR Pfam; PF02201; SWIB; 1.  
 DR Pfam; PF00641; zf-RanBP; 1.  
 DR SMART; SM00184; RING; 1.



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DR PROSITE; PS01358; ZF_RANBP2_1; 1.
DR PROSITE; PS0199; ZF_RANBP2_2; 1.
DR PROSITE; PS0089; ZF_RING_2; 1.
SQ SEQUENCE 436 AA; 49248 MW; 3CBF5E8E98BC4203A CRC64;

Query Match          89.2%; Score 495; DB 2; Length 436;
Best Local Similarity 92.4%; Pred. No. 3e-44; 5; Indels 0; Gaps 0;
Matches 97; Conservative 3; Mismatches 0;

QY 1 SQIPASEQETLVRPRLKLLKLSVGAQKDTYTMKEVLYLQGYIMTKRLYDEKQHIHVH 60
Db 17 SQIPASEQETLVRPRLKLLKLSVGAQKDTYTMKEVLYLQGYIMTKRLYDEKQHIHV 76
QY 61 CSNDLLGLDFGVPSVSKHKRIYTMIVRNLYVNVNQESDSDSGTS 105
Db 77 CSNDLLGLDFGVPSVSKHKRIYTMIVRNLYVNVNQESDSDSGTS 121

RESULT 12
MDM2_MOUSE
ID MDM2_MOUSE STANDARD; PRT; 489 AA.
AC P23804; Q61040; Q64330;
DT 01-NOV-1991 (Rel. 20, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein
DE Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein).
GN Name=Mdm2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A. (ISOFORM MDM2-P90).
RX MEDLINE=91224107; PubMed=2026149;
RA Fakhrazadeh S.S., Trusko S.P., George D.L.;
RT "Tumorigenic potential associated with enhanced expression of a gene
RT that is amplified in a mouse tumor cell line.";
RL EMBO J. 10:1565-1569 (1991).
[2]
RP SEQUENCE FROM N.A. (ISOFORM MDM2-P90).
RX STRAIN=129/Sv;
RC MEDLINE=97074674; PubMed=8917101;
RA Jones S.N., Ansari-Lari M.A., Hancock A.R., Jones W.J., Gibbs R.A.,
RA Donehower L.A., Bradley A.;
RT "Genomic organization of the mouse double minute 2 gene.";
RL Gene 175:209-213 (1996).
[3]
RP SEQUENCE FROM N.A. (ISOFORM MDM2-P90).
RC STRAIN=129/Sv;
RX MEDLINE=96299630; PubMed=8660994;
RA de Oca Luna R.M., Tabor A.D., Eberspaecher H., Hulboy D.L.,
RA Worth L.L., Colman M.S., Finlay C.A., Lozano G.;
RT "The organization and expression of the mdm2 gene.";
RL Genomics 33:352-357 (1996).
[4]
RP SEQUENCE FROM N.A. (ISOFORMS MDM2-P90 AND MDM2-P76).
RX MEDLINE=99175199; PubMed=10075719;
RA Saucedo L.J., Myers C.D., Perry M.E.;
RT "Multiple murine double minute gene 2 (MDM2) proteins are induced by
RT ultraviolet light.";
RL J. Biol. Chem. 274:8161-8168 (1999).
[5]
RP NUCLEOLAR LOCALIZATION SIGNAL.
RX MEDLINE=20180080; PubMed=10713175;
RA Weber J.D., Kuo M.-L., Bothner B., DiGiammarino E.L., Kriwacki R.W.,
RA Rousset M.F., Sherr C.J.;
RT "Cooperative signals governing ARF-mdm2 interaction and nucleolar
RT localization of the complex.";
RL Mol. Cell. Biol. 20:2517-2528 (2000).
[6]
RP PHOSPHORYLATION BY ATM.
RX MEDLINE=20079591; PubMed=10611322;

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RA Khosravi R., Maya R., Gottlieb T., Oren M., Shiloh Y., Shkedy D.;
RT "Rapid ATM-dependent phosphorylation of MDM2 precedes p53 accumulation
RT in response to DNA damage.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:14973-14977 (1999).
CC -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and
CC apoptosis by binding its transcriptional activation domain.
CC Functions as a ubiquitin ligase E3, in the presence of E1 and E2,
CC toward p53 and itself. Permits the nuclear export of p53 and
CC targets it for proteasome-mediated proteolysis.
CC -!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity.
CC -!- SUBUNIT: Binds p53, p73, ARF(P14), ribosomal protein L5 and
CC specifically to RNA. Can interact also with retinoblastoma protein
CC (RB), E1A-associated protein EP300 and the E2F1 transcription
CC factor.
CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed
CC predominantly in the nucleoplasm. Interaction with ARF(P14)
CC results in the localization of both proteins to the nucleolus. The
CC nucleolar localization signals in both ARF(P14) and MDM2 may be
CC necessary to allow efficient nucleolar localization of both
CC proteins.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Mdm2-p90;
CC IsoId=P23804-1; Sequence=Displayed;
CC Note=Isoform Mdm2-p76 can also be produced by alternative
CC initiation at Met-50 of isoform Mdm2-p90, but is produced more
CC efficiently by alternative splicing;
CC Name=Mdm2-p76;
CC IsoId=P23804-2; Sequence=VSP_003215;
CC Note=Does not bind to p53;
CC Event=Alternative initiation;
CC Comment=2 isoforms, Mdm2-p90 (shown here) and Mdm2-p76, are
CC produced by alternative initiation at Met-1 and Met-50. Isoform
CC Mdm2-p76 is produced more efficiently by alternative splicing;
CC -!- TISSUE SPECIFICITY: Ubiquitously expressed at low-level throughout
CC embryo development and in adult tissues. MDM2-p90 is much more
CC abundant than MDM2-p76 in testis, brain, heart, and kidney, but in
CC the thymus, spleen, and intestine, the levels of the MDM2 proteins
CC are roughly equivalent.
CC -!- INDUCTION: By UV light.
CC -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its
CC G1 arrest and apoptosis functions. It also binds p73 and E2F1.
CC Region II contains most of a central acidic region required for
CC interaction with ribosomal protein L5 and a putative C4-type zinc
CC finger. The RING finger domain which coordinates two molecules of
CC zinc interacts specifically with RNA whether or not zinc is
CC present and mediates the hetero-oligomerization with MDM4. It is
CC also essential for its ubiquitin ligase E3 activity toward p53 and
CC itself.
CC -!- PTM: Phosphorylated in response to ionizing radiation in an ATM-
CC dependent manner.
CC -!- DISEASE: The gene for this protein is amplified in a mouse tumor
CC cell line.
CC -!- SIMILARITY: Belongs to the MDM2 / MDM4 family.
CC -!- SIMILARITY: Contains 1 RanBP2-type zinc finger.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC -!- SIMILARITY: Contains 1 SWIB domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X58876; CAA41684.1; -
CC EMBL; U40145; AAA91167.1; -
CC EMBL; U47944; AAB09030.1; -
CC EMBL; U47935; AAB09030.1; JOINED.
CC EMBL; U47936; AAB09030.1; JOINED.
CC EMBL; U47937; AAB09030.1; JOINED.
CC EMBL; U47938; AAB09030.1; JOINED.

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DR EMBL; U47939; AAB09030.1; JOINED.
DR EMBL; U47940; AAB09030.1; JOINED.
DR EMBL; U47941; AAB09030.1; JOINED.
DR EMBL; U47942; AAB09030.1; JOINED.
DR EMBL; U47943; AAB09030.1; JOINED.
DR EMBL; U47934; AAB09031.1; -.
DR PIR; S15349; S15349.
DR HSP; Q9UMT8; 1YCE.
DR MGI; MGI:96952; Mdm2.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IDA.
DR GO; GO:0030163; P:protein catabolism; IDA.
DR GO; GO:0036567; P:protein ubiquitination; IDA.
DR GO; GO:0007089; P:traversing start control point of mitotic c. . .; IDA.
DR InterPro; IPR010984; MDM2.
DR InterPro; IPR003121; SWIB.
DR InterPro; IPR001876; Znf RangDP.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF02201; SWIB; 1.
DR Pfam; PF00641; Zf-RanBP; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01358; ZF_RANBP2_1; 1.
DR PROSITE; PS0199; ZF_RANBP2_2; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS00089; ZF_RING_2; 1.
KW Alternative initiation; Alternative splicing; Ligase; Metal-binding;
KW Nuclear protein; Phosphorylation; Proto-oncogene;
KW Ub1 conjugation pathway; Zinc; Zinc-finger.
FT CHAIN 1 489
FT     ubiquitin-protein ligase E3 Mdm2, isoform
FT     Mdm2-p90.
FT CHAIN 50 489
FT     ubiquitin-protein ligase E3 Mdm2, isoform
FT     Mdm2-p76.
FT     For isoform Mdm2-p76.
FT INIT MET 50 50
FT DOMAIN 27 107
FT     SWIB.
FT DOMAIN 176 182
FT     Nuclear localization signal (Potential).
FT DOMAIN 183 195
FT     Nuclear export signal.
FT DOMAIN 203 213
FT     Poly-Ser.
FT DOMAIN 208 302
FT     ASP-binding.
FT DOMAIN 240 329
FT     Region II.
FT DOMAIN 221 299
FT     Asp/Glu-rich (acidic).
FT ZN FING 297 326
FT     RanBP2-type.
FT ZN FING 436 477
FT     RING-type.
FT DOMAIN 464 471
FT     Nucleolar localization signal
FT     (Potential).
FT VARSP LIC 1 49
FT     Missing (in isoform Mdm2-p76).
FT     /FTIDEVSP 003215.
FT CONFLICT 203 203
FT     S -> T (in Ref. 1).
FT CONFLICT 419 419
FT     D -> H (in Ref. 1).
FT CONFLICT 486 486
FT     S -> T (in Ref. 3).
SQ SEQUENCE 489 AA; 54543 MW; 4ABF489E92038DF4 CRC64;

Query Match 87.5%; Score 485.5; DB 1; Length 489;
Best Local Similarity 86.2%; Pred. No. 3.6e-43;
Matches 94; Conservative 9; Mismatches 3; Indels 3; Gaps 1;

QY 1 SQIPASEQETLVRPKPLLLKLLKSGCAQKDTYMTKVELVYLGQYIMTKELYDEKQOHVH 60
DB 17 SQIPASEQETLVRPKPLLLKLLKSGCAQNDTYMTKREIIYIGYIMTKELYDEKQOHVY 76

QY 61 CSNDLLGDLFGVPSFVSFKHRIYTYMYRNVLVVNQESDSGTSVSEN 109
DB 77 CSNDLLGDLFGVPSFVSFKHRIYMYRNVLVAVSQ---DSGTSLSNS 122

RESULT 13
Q91XK7 PRELIMINARY; PRT; 489 AA.
AC Q91XK7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Mus musculus adult male lung cdna, RIKEN full-length enriched library,

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DE clone:1200011P22 product:transformed mouse 3T3 cell double minute 2,
DE full insert sequence (transformed mouse 3T3 cell double minute 2) (Mus
DE musculus 2 days neonate thymus thymic cells cdna, RIKEN full-length
DE enriched library, clone:E430022B10 product:transformed mouse 3T3 cell
DE double minute 2, full insert sequence).
GN Name=Mdm2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;
RX MEDLINE=24099374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RT Submitted (JUL-2000) to the EMBL/GenBank/DDJ databases.
RN [7]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Mouse;

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RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,  
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [18]  
 RC STRAIN=C57BL/6; TISSUE=Mouse;  
 RA Strausberg R.;  
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
 RN [19]  
 RC SEQUENCE FROM N.A.  
 RP STRAIN=NOD; TISSUE=Thymus;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
 RA Saio R., Saichon H., Sakai K., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akashira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK004719; BAB23502.1; -;  
 DR EMBL; BC050902; AAH50902.1; -;  
 DR EMBL; BC050902; AAH50902.1; -;  
 DR HSSP; Q9UMT8; 1YCR.  
 DR MGD; MGI:96952; Mdm2.  
 DR GO; GO:0005730; C:nucleolus; IDA.  
 DR GO; GO:0005515; F:protein binding; IPI.  
 DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IDA.  
 DR GO; GO:0030163; P:protein catabolism; IDA.  
 DR GO; GO:0016567; P:protein ubiquitination; IDA.  
 DR GO; GO:0007089; P:traversing start control point of mitotic c. . .; IDA.  
 DR InterPro; IPR010984; MDM2.  
 DR InterPro; IPR003121; SWIB\_MDM2.  
 DR InterPro; IPR001876; Znf\_RANGDP.  
 DR Pfam; PF02201; SWIB; 1.  
 DR Pfam; PF00641; zf-RanBP; 1.  
 DR SMART; SM00184; RING; 1.  
 DR PROSITE; PS01358; ZF\_RANBP2\_1; 1.  
 DR PROSITE; PS01399; ZF\_RANBP2\_2; 1.  
 DR PROSITE; PS00889; ZF\_RANBP2\_1; 1.  
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 Query Match 87.5%; Score 485.5; DB 2; Length 489;  
 Best Local Similarity 86.2%; Pred. No. 3.6e-43;  
 Matches 94; Conservative 9; Mismatches 3; Indels 3; Gaps 1;  
 QY 1 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLVYLQYIMTKRLYDEKQOQHVH 60  
 DB 17 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLVYLQYIMTKRLYDEKQOQHV 76  
 QY 61 CSNDLLGLDGLFGVPSFVSKHRKIYTMIRNLV 109

Db 77 CSNDLLGLDGLFGVPSFVSKHRKIYTMIRNLVAVSQQ---DSGTSLS 122  
 RESULT 14  
 ID Q8WYJ3 PRELIMINARY; PRT; 118 AA.  
 AC Q8WYJ3;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE MDM2 protein (Fragment).  
 GN Name=MDM2;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21248713; PubMed=11351297;  
 RA Tamborini E., Della Torre G., Lavarino C., Azzarelli A.,  
 RA Carpinelli P., Pierotti M.A., Pilotti S.;  
 RT "Analysis of the molecular species generated by MDM2 gene  
 RT amplification in liposarcomas";  
 RL Int. J. Cancer 92:790-796 (2001).  
 DR EMBL; AF092843; AAL40178.1; -;  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR InterPro; IPR010984; MDM2.  
 DR InterPro; IPR003121; SWIB\_MDM2.  
 DR Pfam; PF02201; SWIB; 1.  
 DR NON\_TER 118  
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 Best Local Similarity 97.8%; Pred. No. 5.1e-42;  
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 DB 17 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLVYLQYIMTKRLYDEKQOQHV 76  
 QY 61 CSNDLLGLDGLFGVPSFVSKHRKIYTMIRNLV 93  
 DB 77 CSNDLLGLDGLFGVPSFVSKHRKIYTMIRNLV 109  
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 ID MDM2\_MESAU STANDARD; PRT; 466 AA.  
 AC Q60524;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein  
 DE Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Fragment).  
 GN Name=MDM2;  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus.  
 OX NCBI\_TaxID=10036;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=Pancreas;  
 RC MEDLINE=95300112; PubMed=7780969;  
 RA Chang K.W., Laconi S., Mangold K.A., Hubchak S., Scarpelli D.G.;  
 RT "Multiple genetic alterations in hamster pancreatic ductal  
 RT adenocarcinomas";  
 RL Cancer Res. 55:2560-2568 (1995).  
 CC -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and  
 CC apoptosis by binding its transcriptional activation domain.  
 CC Functions as a ubiquitin ligase E3, in the presence of E1 and E2,  
 CC toward p53 and itself. Permits the nuclear export of p53 and



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OM protein - protein search, using sw model

Run on: January 27, 2005, 17:54:26 ; Search time 22.2 Seconds  
(without alignments)  
325.615 Million cell updates/sec

Title: US-10-822-254-10  
Perfect score: 555  
Sequence: 1 SQIPASEQETLVRPKPLLK.....NLVVNQESSDSTGTSVSEN 109

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/iaa/5B COMB.pgp:\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pgp:\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pgp:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pgp:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pgp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	545	98.2	188	US-09-603-052-4	Sequence 4, Appli
2	545	98.2	491	US-07-903-103-2	Sequence 2, Appli
3	545	98.2	491	US-08-044-619A-2	Sequence 2, Appli
4	545	98.2	491	US-08-283-911-2	Sequence 2, Appli
5	545	98.2	491	US-08-245-500A-3	Sequence 3, Appli
6	545	98.2	491	US-08-390-546-3	Sequence 3, Appli
7	545	98.2	491	US-08-390-479A-3	Sequence 3, Appli
8	545	98.2	491	US-08-557-393-3	Sequence 3, Appli
9	545	98.2	491	US-08-390-516C-3	Sequence 3, Appli
10	545	98.2	491	US-08-390-517A-3	Sequence 3, Appli
11	545	98.2	491	US-08-390-515A-3	Sequence 3, Appli
12	545	98.2	491	US-08-801-718-3	Sequence 3, Appli
13	545	98.2	491	US-09-170-159A-3	Sequence 3, Appli
14	545	98.2	491	US-09-480-718-44	Sequence 44, Appli
15	528.5	95.2	216	US-09-510-252-4	Sequence 4, Appli
16	485.5	87.5	489	US-07-903-103-4	Sequence 4, Appli
17	485.5	87.5	489	US-08-044-619A-4	Sequence 4, Appli
18	485.5	87.5	489	US-08-283-911-4	Sequence 4, Appli
19	485.5	87.5	489	US-08-245-500A-5	Sequence 5, Appli
20	485.5	87.5	489	US-08-390-546-5	Sequence 5, Appli
21	485.5	87.5	489	US-08-390-479A-5	Sequence 5, Appli
22	485.5	87.5	489	US-08-557-393-5	Sequence 5, Appli
23	485.5	87.5	489	US-08-390-516C-5	Sequence 5, Appli
24	485.5	87.5	489	US-08-390-517A-5	Sequence 5, Appli
25	485.5	87.5	489	US-08-390-515A-5	Sequence 5, Appli
26	485.5	87.5	489	US-08-801-718-5	Sequence 5, Appli
27	485.5	87.5	489	US-09-170-159A-5	Sequence 5, Appli

28	485.5	87.5	489	4	US-09-480-718-46	Sequence 46, Appli
29	176	31.7	243	4	US-09-786-702-2	Sequence 2, Appli
30	73.5	13.2	244	4	US-09-543-681A-6675	Sequence 6675, Ap
31	71.5	12.9	420	4	US-09-270-767-43304	Sequence 43304, A
32	66.5	12.0	104	4	US-09-270-767-41801	Sequence 41801, A
33	66.5	12.0	590	3	US-09-232-191-25	Sequence 25, Appli
34	66.5	12.0	590	3	US-09-232-200-75	Sequence 75, Appli
35	66.5	12.0	590	3	US-09-232-197-75	Sequence 75, Appli
36	66.5	12.0	590	3	US-09-232-201-75	Sequence 75, Appli
37	66.5	12.0	590	3	US-09-232-195-75	Sequence 75, Appli
38	65	11.7	384	4	US-08-504-617-2	Sequence 2, Appli
39	65	11.7	766	4	US-09-248-796A-16626	Sequence 16626, A
40	64.5	11.6	253	4	US-09-270-767-38412	Sequence 38412, A
41	64.5	11.6	253	4	US-09-270-767-53629	Sequence 53629, A
42	64.5	11.6	482	4	US-09-248-796A-17755	Sequence 17755, A
43	64.5	11.6	1432	3	US-08-781-891-71	Sequence 71, Appli
44	64.5	11.6	1432	4	US-09-618-166-71	Sequence 71, Appli
45	64.5	11.6	2184	4	US-09-417-485D-6	Sequence 6, Appli

## ALIGNMENTS

RESULT 1  
US-09-603-052-4  
; Sequence 4, Application US/09603052  
; Patent No. 6492116  
; GENERAL INFORMATION:  
; APPLICANT: Chene, Patrick  
; APPLICANT: Hochkeppel, Heinz-Kurt  
; TITLE OF INVENTION: Assay for identifying inhibitors of the interaction  
; FILE REFERENCE: between proteins p53 and dm2  
; CURRENT APPLICATION NUMBER: US/09/603,052  
; CURRENT FILING DATE: 2000-06-26  
; PRIOR APPLICATION NUMBER: EP 95810576.9  
; PRIOR FILING DATE: 1995-09-18  
; PRIOR APPLICATION NUMBER: PCT/EP96/03957  
; PRIOR FILING DATE: 1996-09-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 188  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-603-052-4

Query Match 98.2%; Score 545; DB 4; Length 188;  
Best Local Similarity 98.2%; Pred. No. 8.4e-60;  
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SQIPASEQETLVRPKPLLKLLKSVGAOKDTYTMKEVLYLGOYIMTKRLYDEKQOHHVH 60  
DB 17 SQIPASEQETLVRPKPLLKLLKSVGAOKDTYTMKEVLYLGOYIMTKRLYDEKQOHHVY 76  
QY 61 CSNDLLGDLFGVPSPSVKHEHKIYTMIRNLVNVNQESSDSTGTSVSEN 109  
DB 77 CSNDLLGDLFGVPSPSVKHEHKIYTMIRNLVNVNQESSDSTGTSVSEN 125

RESULT 2  
US-07-903-103-2  
; Sequence 2, Application US/07903103  
; Patent No. 5411860  
; GENERAL INFORMATION:  
; APPLICANT: VOGELSTEIN, BERT  
; APPLICANT: KINZLER, KENNETH  
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
; TITLE OF INVENTION: HUMAN TUMORS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
; STREET: 1001 G ST., N.W.

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; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/903,103
; FILING DATE: 19920623
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/867,840
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.40148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-903-103-2

Query Match      98.2%; Score 545; DB 1; Length 491;
Best Local Similarity 98.2%; Pred. No. 3e-59;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVH 60
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVY 76
Oy 61 CSNDLLGDLFGVPSFVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 109
Db 77 CSNDLLGDLFGVPSFVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 125

RESULT 3
US-08-044-619A-2
; Sequence 2, Application US/08044619A
; Patent No. 5420263
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY
; APPLICANT: 720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G ST., N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/044,619A
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/903,103

; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 07/903,103
; FILING DATE: 23-JUN-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/867,840
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.40148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-044-619A-2

Query Match      98.2%; Score 545; DB 1; Length 491;
Best Local Similarity 98.2%; Pred. No. 3e-59;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVH 60
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVY 76
Oy 61 CSNDLLGDLFGVPSFVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 109
Db 77 CSNDLLGDLFGVPSFVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 125

RESULT 4
US-08-283-911-2
; Sequence 2, Application US/08283911
; Patent No. 5519118
; GENERAL INFORMATION:
; APPLICANT: VOGELSTEIN, BERT
; APPLICANT: KINZLER, KENNETH
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G ST., N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/283,911
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/903,103
; FILING DATE: 23-JUN-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/867,840
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.40148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-283-911-2

Query Match      98.2%; Score 545; DB 1; Length 491;
Best Local Similarity 98.2%; Pred. No. 3e-59;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGYQYIMTKRLYDEKQOHIVH 60
        |||||||
Db      17 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGYQYIMTKRLYDEKQOHIVY 76
        |||||||

Qy      61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVNNQESSDGSSTSVSEN 109
        |||||||
Db      77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVNNQESSDGSSTSVSEN 125
        |||||||

RESULT 5
US-08-245-500A-3
; Sequence 3, Application US/08245500A
; Patent No. 5550023
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/245.500A
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-245-500A-3

Query Match      98.2%; Score 545; DB 1; Length 491;
Best Local Similarity 98.2%; Pred. No. 3e-59;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGYQYIMTKRLYDEKQOHIVH 60
        |||||||
Db      17 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGYQYIMTKRLYDEKQOHIVY 76
        |||||||

Qy      61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVNNQESSDGSSTSVSEN 109
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Db      77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVNNQESSDGSSTSVSEN 125
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RESULT 6
US-08-390-546-3
; Sequence 3, Application US/08390546
; Patent No. 5606044
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390.546
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-390-546-3

Query Match      98.2%; Score 545; DB 1; Length 491;
Best Local Similarity 98.2%; Pred. No. 3e-59;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGYQYIMTKRLYDEKQOHIVH 60
        |||||||
Db      17 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGYQYIMTKRLYDEKQOHIVY 76
        |||||||

Qy      61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVNNQESSDGSSTSVSEN 109
        |||||||
Db      77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVNNQESSDGSSTSVSEN 125
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RESULT 7
US-08-390-479A-3
; Sequence 3, Application US/08390479A
; Patent No. 5618921
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
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Fri Jan 28 09:36:23 2005

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/
/ ADDRESSEE: BANNER & WITCOFF, LTD.
/ STREET: 1001 G STREET, N.W.
/ CITY: WASHINGTON
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20001
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/390,479A
/ FILING DATE: 02-FEB-1995
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: KAGAN, SARAH A.
/ REGISTRATION NUMBER: 32,141
/ REFERENCE/DOCKET NUMBER: 01107.48992
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-508-9100
/ TELEFAX: 202-508-9299
/ TELEX: 197430 BBMB UT
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 491 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-390-479A-3

Query Match      98.2%; Score 545; DB 1; Length 491;
Best Local Similarity 98.2%; Pred. No. 3e-59;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1  SOIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQKHIVH 60
Db      17  SOIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQKHIVY 76

QY      61  CSNDLLGDLFGVPSPFSVKEHRKIYTYMYRNLVVNVNQESSDSGTSVSEN 109
Db      77  CSNDLLGDLFGVPSPFSVKEHRKIYTYMYRNLVVNVNQESSDSGTSVSEN 125

RESULT 8
US-08-557-393-3
/ Sequence 3, Application US/08557393
/ Patent No. 5702903
/ GENERAL INFORMATION:
/ APPLICANT: BURRELL, MARILEE
/ APPLICANT: HILL, DAVID E.
/ APPLICANT: KINZLER, KENNETH W.
/ APPLICANT: VOGELSTEIN, BERT
/ TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
/ TITLE OF INVENTION: HUMAN TUMORS
/ NUMBER OF SEQUENCES: 5
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
/ STREET: 1001 G STREET, N.W.
/ CITY: WASHINGTON
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20001
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/557,393
/ FILING DATE: 13-NOV-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:

/
/ ADDRESSEE: BANNER & WITCOFF, LTD.
/ STREET: 1001 G STREET, N.W.
/ CITY: WASHINGTON
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20001
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/390,479A
/ FILING DATE: 02-FEB-1995
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: KAGAN, SARAH A.
/ REGISTRATION NUMBER: 32,141
/ REFERENCE/DOCKET NUMBER: 01107.48992
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-508-9100
/ TELEFAX: 202-508-9299
/ TELEX: 197430 BBMB UT
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 491 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-390-479A-3

Query Match      98.2%; Score 545; DB 1; Length 491;
Best Local Similarity 98.2%; Pred. No. 3e-59;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1  SOIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQKHIVH 60
Db      17  SOIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQKHIVY 76

QY      61  CSNDLLGDLFGVPSPFSVKEHRKIYTYMYRNLVVNVNQESSDSGTSVSEN 109
Db      77  CSNDLLGDLFGVPSPFSVKEHRKIYTYMYRNLVVNVNQESSDSGTSVSEN 125

RESULT 9
US-08-390-516C-3
/ Sequence 3, Application US/08390516C
/ Patent No. 5708136
/ GENERAL INFORMATION:
/ APPLICANT: BURRELL, MARILEE
/ APPLICANT: HILL, DAVID E.
/ APPLICANT: KINZLER, KENNETH W.
/ APPLICANT: VOGELSTEIN, BERT
/ TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
/ TITLE OF INVENTION: HUMAN TUMORS
/ NUMBER OF SEQUENCES: 9
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
/ STREET: 1001 G STREET, N.W.
/ CITY: WASHINGTON
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20001
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/390,516C
/ FILING DATE: 07-APR-1993
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: KAGAN, SARAH A.
/ REGISTRATION NUMBER: 32,141
/ REFERENCE/DOCKET NUMBER: 01107.42798
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-508-9100
/ TELEFAX: 202-508-9299
/ TELEX: 197430 BBMB UT
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 491 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-557-393-3
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## US-08-390-516C-3

Query Match 98.2%; Score 545; DB 1; Length 491;  
Best Local Similarity 98.2%; Pred. No. 3e-59;  
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLVYILGOYIMTKRLYDEKQOHHVH 60  
Db 17 SQIPASEQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLVYILGOYIMTKRLYDEKQOHHVY 76

Qy 61 CSNDLLGLDFGVPSFSVKEHRKIYTMIRNVLVNVNQSSDSGTSVSEN 109  
Db 77 CSNDLLGLDFGVPSFSVKEHRKIYTMIRNVLVNVNQSSDSGTSVSEN 125

## RESULT 10

US-08-390-517A-3  
; Sequence 3, Application US/08390517A  
; Patent No. 5736338  
; GENERAL INFORMATION:  
; APPLICANT: BURRELL, MARILEE  
; APPLICANT: HILL, DAVID E.  
; APPLICANT: KINZLER, KENNETH W.  
; APPLICANT: VOGELSTEIN, BERT  
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
; TITLE OF INVENTION: HUMAN TUMORS  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
; STREET: 1001 G STREET, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20001

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,517A  
FILING DATE: 07-APR-1993  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: KAGAN, SARAH A.  
REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 01107.42798  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299  
TELEX: 197430 BBMB UT

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 491 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

## US-08-390-517A-3

Query Match 98.2%; Score 545; DB 1; Length 491;  
Best Local Similarity 98.2%; Pred. No. 3e-59;  
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLVYILGOYIMTKRLYDEKQOHHVH 60  
Db 17 SQIPASEQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLVYILGOYIMTKRLYDEKQOHHVY 76

Qy 61 CSNDLLGLDFGVPSFSVKEHRKIYTMIRNVLVNVNQSSDSGTSVSEN 109  
Db 77 CSNDLLGLDFGVPSFSVKEHRKIYTMIRNVLVNVNQSSDSGTSVSEN 125

## RESULT 11

## US-08-390-515A-3

; Sequence 3, Application US/08390515A  
; Patent No. 5756455  
; GENERAL INFORMATION:  
; APPLICANT: BURRELL, MARILEE  
; APPLICANT: HILL, DAVID E.  
; APPLICANT: KINZLER, KENNETH W.  
; APPLICANT: VOGELSTEIN, BERT  
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
; TITLE OF INVENTION: HUMAN TUMORS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
; STREET: 1001 G STREET, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20001

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,515A  
FILING DATE: 07-APR-1993  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: KAGAN, SARAH A.  
REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 01107.42798  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299  
TELEX: 197430 BBMB UT

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 491 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

## US-08-390-515A-3

Query Match 98.2%; Score 545; DB 1; Length 491;  
Best Local Similarity 98.2%; Pred. No. 3e-59;  
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLVYILGOYIMTKRLYDEKQOHHVH 60  
Db 17 SQIPASEQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLVYILGOYIMTKRLYDEKQOHHVY 76

Qy 61 CSNDLLGLDFGVPSFSVKEHRKIYTMIRNVLVNVNQSSDSGTSVSEN 109  
Db 77 CSNDLLGLDFGVPSFSVKEHRKIYTMIRNVLVNVNQSSDSGTSVSEN 125

## RESULT 12

US-08-801-718-3  
; Sequence 3, Application US/08801718  
; Patent No. 5858976  
; GENERAL INFORMATION:  
; APPLICANT: BURRELL, MARILEE  
; APPLICANT: HILL, DAVID E.  
; APPLICANT: KINZLER, KENNETH W.  
; APPLICANT: VOGELSTEIN, BERT  
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
; TITLE OF INVENTION: HUMAN TUMORS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
; STREET: 1001 G STREET, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.

COUNTRY: USA  
ZIP: 20001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/08/801,718  
FILING DATE: 14-FEB-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/390,515  
FILING DATE: 07-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KAGAN, SARAH A.  
REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 01107.42798  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 491 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-801-718-3

Query Match 98.2%; Score 545; DB 2; Length 491;  
Best Local Similarity 98.2%; Pred. No. 3e-59;  
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKLLKLLKSVGAQKDTYTMKEVLYYLQYIMTKRLYDEKQOHIVH 60  
Db 17 SQIPASEQETLVRPKLLKLLKSVGAQKDTYTMKEVLYYLQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPSPSVKHEHKIYTMIRNLVVNNQSSDSGTSVSEN 109  
Db 77 CSNDLLGDLFGVPSPSVKHEHKIYTMIRNLVVNNQSSDSGTSVSEN 125

RESULT 13  
US-09-170-159A-3  
Sequence 3, Application US/09170159A  
Patent No. 6399755  
GENERAL INFORMATION:  
APPLICANT: BURRELL, MARILEE  
HILL, DAVID E.  
KINZLER, KENNETH W.  
VOGELSTEIN, BERT  
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
HUMAN TUMORS  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
STREET: 1001 G STREET, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/170,159A  
FILING DATE: 13-Oct-1998  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: KAGAN, SARAH A.

COUNTRY: USA  
ZIP: 20001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/08/801,718  
FILING DATE: 14-FEB-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/390,515  
FILING DATE: 07-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KAGAN, SARAH A.  
REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 01107.42798  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 491 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-480-718-44

Query Match 98.2%; Score 545; DB 3; Length 491;  
Best Local Similarity 98.2%; Pred. No. 3e-59;  
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKLLKLLKSVGAQKDTYTMKEVLYYLQYIMTKRLYDEKQOHIVH 60  
Db 17 SQIPASEQETLVRPKLLKLLKSVGAQKDTYTMKEVLYYLQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPSPSVKHEHKIYTMIRNLVVNNQSSDSGTSVSEN 109  
Db 77 CSNDLLGDLFGVPSPSVKHEHKIYTMIRNLVVNNQSSDSGTSVSEN 125

RESULT 14  
US-09-480-718-44  
Sequence 44, Application US/09480718  
Patent No. 6407062  
GENERAL INFORMATION:  
APPLICANT: Sherr, Charles J  
APPLICANT: Queller, Dawn E  
APPLICANT: Weber, Jason D  
APPLICANT: Rousssel, Martine F  
APPLICANT: Frederique, Zindy  
TITLE OF INVENTION: ARF-19, A NOVEL REGULATOR OF THE MAMMALIAN CELL CYCLE  
FILE REFERENCE: 1340-1-023 CIP 1  
CURRENT APPLICATION NUMBER: US/09/480,718  
CURRENT FILING DATE: 2000-01-07  
EARLIER APPLICATION NUMBER: 09/129,855  
EARLIER FILING DATE: 1998-08-06  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 44  
LENGTH: 491  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-480-718-44

Query Match 98.2%; Score 545; DB 4; Length 491;  
Best Local Similarity 98.2%; Pred. No. 3e-59;  
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Db 17 SQIPASEQETLVRPKLLKLLKSVGAQKDTYTMKEVLYYLQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPSPSVKHEHKIYTMIRNLVVNNQSSDSGTSVSEN 109  
Db 77 CSNDLLGDLFGVPSPSVKHEHKIYTMIRNLVVNNQSSDSGTSVSEN 125

RESULT 15  
US-09-510-252-4  
Sequence 4, Application US/09510252  
Patent No. 6372490  
GENERAL INFORMATION:  
APPLICANT: Nandabalan, Krishnan  
APPLICANT: Yang, Meijia  
APPLICANT: Schulz, Vincent

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; APPLICANT: Curagen Corporation
; TITLE OF INVENTION: MDM INTERACTING PROTEIN AND METHODS OF USE THEREOF
; FILE REFERENCE: 15966-524 MDM US
; CURRENT APPLICATION NUMBER: US/09/510,252
; CURRENT FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: USSN 60/121,192
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: USSN 60/122,643
; PRIOR FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-510-252-4

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Best Local Similarity 97.2%; Pred. No. 1.1e-57;
Matches 106; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

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Db      17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYL-QYIMTKRLYDEKQQHIVY 75

Qy      61 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVVNQOESSDSGTSVSEN 109
Db      76 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVVNQOESSDSGTSVSEN 124
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:59:36 ; Search time 69.4 Seconds

(without alignments)  
567.443 Million cell updates/sec

Title: US-10-822-254-10

Perfect score: 555

Sequence: 1 SQIPASEQETLVRPKPLLLK.....NLVVNQESSDSGTSVSEN 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum Match 100%

Listing first 45 summaries

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*

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- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
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- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	ID	Description
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2	545	98.2	491	9	US-09-888-077-1 Sequence 2, Appli
3	545	98.2	491	10	US-09-029-327-2 Sequence 8, Appli
4	545	98.2	491	11	US-09-966-724-2 Sequence 2, Appli
5	545	98.2	491	15	US-10-422-536-137 Sequence 137, App
6	545	98.2	491	15	US-10-232-951-35 Sequence 35, App
7	545	98.2	491	17	US-10-685-838-1 Sequence 1, Appli
8	545	98.2	491	17	US-10-724-225-2 Sequence 2, Appli
9	545	98.2	491	17	US-10-489-802-8 Sequence 8, Appli
10	545	98.2	491	17	US-10-723-860-2236 Sequence 4, Appli
11	528.5	95.2	216	13	US-10-057-510-4 Sequence 380, App
12	519.5	93.6	522	15	US-10-287-226-380 Sequence 382, App
13	519.5	93.6	522	15	US-10-287-226-382

14	485.5	87.5	489	9	US-09-956-425-6 Sequence 6, Appli
15	485.5	87.5	489	11	US-09-966-724-4 Sequence 4, Appli
16	485.5	87.5	489	11	US-10-489-802-6 Sequence 6, Appli
17	478	86.1	95	17	US-10-685-838-2 Sequence 2, Appli
18	469	84.5	95	17	US-10-685-838-4 Sequence 4, Appli
19	465	83.8	92	17	US-10-685-838-3 Sequence 3, Appli
20	306	55.1	59	14	US-10-211-088-143 Sequence 143, App
21	74.5	13.4	578	16	US-10-437-963-174237 Sequence 174237, App
22	73	13.2	613	16	US-10-437-963-113326 Sequence 113326, App
23	72	13.0	967	15	US-10-282-122A-59020 Sequence 59020, A
24	71	12.8	472	14	US-10-369-493-16585 Sequence 16585, A
25	71	12.8	473	15	US-10-282-122A-45311 Sequence 45311, A
26	70.5	12.7	467	14	US-10-362-774-3 Sequence 3, Appli
27	70.5	12.6	467	14	US-10-369-493-6071 Sequence 6071, Ap
28	70	12.6	969	15	US-10-335-977-7409 Sequence 7409, Ap
29	70	12.6	972	15	US-10-335-977-7410 Sequence 7410, Ap
30	69.5	12.5	328	17	US-10-425-115-191466 Sequence 191466, App
31	69.5	12.5	438	10	US-09-769-787-48 Sequence 48, Appl
32	69.5	12.5	709	15	US-10-282-122A-63455 Sequence 63455, A
33	68	12.3	383	15	US-10-424-599-282528 Sequence 282528, App
34	68	12.3	438	14	US-10-176-584A-2 Sequence 2, Appli
35	68	12.3	705	15	US-10-425-114-57081 Sequence 57081, A
36	68	12.3	705	17	US-10-425-115-365082 Sequence 365082, App
37	67.5	12.2	79	15	US-10-424-599-236213 Sequence 236213, A
38	67.5	12.2	291	15	US-10-425-114-59572 Sequence 59572, A
39	67.5	12.2	291	17	US-10-425-115-191465 Sequence 191465, App
40	67.5	12.2	350	10	US-09-746-783-54 Sequence 54, Appl
41	67.5	12.2	422	14	US-10-369-493-7027 Sequence 7027, Ap
42	67.5	12.2	837	16	US-10-408-765A-2452 Sequence 2452, Ap
43	67	12.1	368	15	US-10-389-566-382 Sequence 382, App
44	66.5	12.0	121	17	US-10-425-115-282854 Sequence 282854, App
45	66.5	12.0	187	17	US-10-425-115-227933 Sequence 227933, App

## ALIGNMENTS

### RESULT 1

US-09-888-077-1  
; Sequence 1, Application US/09888077  
; Patent No. US20020031818A1  
; GENERAL INFORMATION:  
; APPLICANT: Ronal, Ze'ev  
; APPLICANT: Fuchs, Serge  
; TITLE OF INVENTION: Modification of Mdm2 Activity  
; FILE REFERENCE: 2420/1H195-US1  
; CURRENT APPLICATION NUMBER: US/09/888,077  
; CURRENT FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: US 60/213,343  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 491  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-888-077-1

Query Match 98.2%; Score 545; DB 9; Length 491;  
Best Local Similarity 98.2%; Pred. No. 2.9e-55;  
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDYTMKEVLVYLQYIMTKRLYDEKQOHVH 60  
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDYTMKEVLVYLQYIMTKRLYDEKQOHVY 76  
Qy 61 CSNDLLGLDGLFGVPFSVKEHRKIYMTIYRNLVNVNQESSDSGTSVSEN 109  
Db 77 CSNDLLGLDGLFGVPFSVKEHRKIYMTIYRNLVNVNQESSDSGTSVSEN 125

### RESULT 2

US-09-956-425-8

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; Sequence 8, Application US/09956425
; Patent No. US20020045192A1
; GENERAL INFORMATION:
; APPLICANT: Kriwacki, Richard
; APPLICANT: Bothner, Brian
; APPLICANT: Lewis, William
; TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and Method of Use Thereof
; FILE REFERENCE: 1340/1/035
; CURRENT APPLICATION NUMBER: US/09/956,425
; CURRENT FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-956-425-8

Query Match          98.2%; Score 545; DB 9; Length 491;
Best Local Similarity 98.2%; Pred. No. 2.9e-55;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLQYIMTKRLYDEKQOHIVH 60
DB 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDLLGDLFGVPSFVKHEHRIYTMIRNLVNVNQESSDSGTSVSEN 109
DB 77 CSNDLLGDLFGVPSFVKHEHRIYTMIRNLVNVNQESSDSGTSVSEN 125

RESULT 3
US-09-029-327-2
; Sequence 2, Application US/09029327
; Publication No. US20030060432A1
; GENERAL INFORMATION:
; APPLICANT: TOCQUE, Bruno
; APPLICANT: WASLYK, Bohdan
; APPLICANT: DUBS-POTERSZMAN,
; APPLICANT: Marie-Christine
; TITLE OF INVENTION: ANTAGONISTS OF THE ONCOGENIC ACTIVITY OF
; TITLE OF INVENTION: THE PROTEIN MDM2, AND USE THEREOF IN THE TREATMENT OF
; TITLE OF INVENTION: CANCERS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, Mailstop 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/029,327
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 96/01340
; FILING DATE: 02-SEP-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO FR95/10331
; FILING DATE: 04-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fehlner Esq., Paul F.
; REGISTRATION NUMBER: 35,135
; REFERENCE/DOCKET NUMBER: ST95050-US
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808

```

```

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-029-327-2

Query Match          98.2%; Score 545; DB 10; Length 491;
Best Local Similarity 98.2%; Pred. No. 2.9e-55;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLQYIMTKRLYDEKQOHIVH 60
DB 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDLLGDLFGVPSFVKHEHRIYTMIRNLVNVNQESSDSGTSVSEN 109
DB 77 CSNDLLGDLFGVPSFVKHEHRIYTMIRNLVNVNQESSDSGTSVSEN 125

RESULT 4
US-09-966-724-2
; Sequence 2, Application US/09966724
; Publication No. US20040170971A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; HUMAN TUMORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G ST., N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/966,724
; FILING DATE: 01-Oct-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/044,619
; FILING DATE: 2001-10-01
; APPLICATION NUMBER: US 07/867,840
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.40148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-3299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
; US-09-966-724-2

Query Match          98.2%; Score 545; DB 11; Length 491;
Best Local Similarity 98.2%; Pred. No. 2.9e-55;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy	1	SOIPASEQETLVVRPKPILLKLLKLVCAQKDTVTMKEVLYYLQGYIMTKRLYDEKQOHIVH	60
Db	17	SOIPASEQETLVVRPKPILLKLLKLVCAQKDTVTMKEVLYYLQGYIMTKRLYDEKQOHIVY	76
Qy	61	CSNDLLGDLFGVPSPFSGVKEHRKIYTIMYRNLVVVAQQESSDGSCTGSVSEN	109
Db	77	CSNDLLGDLFGVPSPFSGVKEHRKIYTIMYRNLVVVAQQESSDGSCTGSVSEN	125

```

RESULT 5
US-10-422-536-137
; Sequence 137, Application US/10422536
; Publication No. US20040014100A1
; GENERAL INFORMATION:
; APPLICANT: Kinsella, Todd
; APPLICANT: Lorens, James
; APPLICANT: Pray, Todd
; APPLICANT: Bennett, Mark
; TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR INHIBITING
; TITLE OF INVENTION: PROTEIN-PROTEIN INTERACTION
; FILE REFERENCE: A-71433-1/AMP/CYO
; CURRENT APPLICATION NUMBER: US/10/422.536
; CURRENT FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: US 60/187,130
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 09/800,770
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: US 10/232,758
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 137
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-422-536-137

```

	Query Match	98.2%	Score 545;	DB 15;	Length 491;
	Best Local Similarity	98.2%;	Pred. No. 2.9e-55;		
	Matches 107;	Conservative 2;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	SOIPASEQETLVRPKP	LLLLLLKLLKSVGAQKDTY	TMKEVLVYLGQYIMTKRLY	YDEKQQHIVH 60
Db	17	SOIPASEQETLVRPKP	LLLLLLKLLKSVGAQKDTY	TMKEVLVYLGQYIMTKRLY	YDEKQQHIVY 76
Qy	61	CSNDLLGLDLFGVPSF	SVKEHRKITYIM	YRNLVVMNQOESSDS	SGTSVSEN 109
Db	77	CSNDLLGLDLFGVPSF	SVKEHRKITYIM	YRNLVVMNQOESSDS	SGTSVSEN 125

```

RESULT 6
US-10-232-951-35
; Sequence 35, Application US/10232951
; Publication No. US20040043386A1
; GENERAL INFORMATION:
; APPLICANT: Pray, Todd
; APPLICANT: Wong, Brian
; APPLICANT: Bennett, Mark
; APPLICANT: Parlati, Francesco
; APPLICANT: Rigel Pharmaceuticals, Incorporated
; TITLE OF INVENTION: Methods and Compositions for Functional Ubiquitin
; TITLE OF INVENTION: Assays
; FILE REFERENCE: 021044-006800US
; CURRENT APPLICATION NUMBER: US/10/232,951
; CURRENT FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: E3 ubiquitin ligating agent mouse double minute 2

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; OTHER INFORMATION: (mdm2) homolog full length protein isoform, mouse
; OTHER INFORMATION: p53-binding protein (MDM2) homolog, transcript
; OTHER INFORMATION: variant MDM2, transformed 3T3 cell double minute 2,
; OTHER INFORMATION: Mdm2 cDNA
US-10-232-951-35

Query Match          98.2%; Score 545; DB 15; Length 491;
Best local Similarity 98.2%; Pred. No. 2.9e-55;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1  SQIPASQETLVRPKPLLLKLLKLLSVGAKDQTYTMKEVLYYLGGQYIMTKRLVDEKQKHIVH 60
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      17  SQIPASQETLVRPKPLLLKLLKLLSVGAKDQTYTMKEVLYYLGGQYIMTKRLVDEKQKHIVY 76

Qy      61  CSNDLLGDLFGVPSFSVKEHKRYTYMIRNLVVMNQOESSDSGTSVSSEN 109
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      77  CSNDLLGDLFGVPSFSVKEHKRYTYMIRNLVVMNQOESSDSGTSVSSEN 125

```

RESULT 7  
US-10-685-838-1  
; Sequence 1, Application US/10685838  
; Publication No. US20040197893A1  
; GENERAL INFORMATION:  
; APPLICANT: SHUBERT, CARSTEN  
; APPLICANT: GRASBERGER, BRUCE  
; APPLICANT: MAGUIRE, DIANE  
; APPLICANT: DECKMAN, INGRID  
; APPLICANT: SPURLINO, JOHN  
; TITLE OF INVENTION: HDM2-INHIBITOR COMPLEXES AND USES THEREOF  
; FILE REFERENCE: PRD-2137-USANP  
; CURRENT APPLICATION NUMBER: US/10/685,838  
; CURRENT FILING DATE: 2003-10-15  
; PRIOR APPLICATION NUMBER: 60/418,350  
; PRIOR FILING DATE: 2002-10-16  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 1  
; LENGTH: 491  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-685-838-1

	Query Match	98.2%	Score 545;	DB 17;	Length 491;
	Best Local Similarity	98.2%;	Pred. No. 2.9e-55;		
	Matches 107;	Conservative 2;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	SQIPASEQETLVRPKPLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQQHIVH	60		
Db	17	SQIPASEQETLVRPKPLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQQHIVY	76		
Qy	61	CSNDLLGDLFGVPSPFSVKEHRKIYTIYRNLVVNNQOESSDSGTGSVEN	109		
Db	77	CSNDLLGDLFGVPSPFSVKEHRKIYTIYRNLVVNNQOESSDSGTGSVEN	125		

RESULT 8  
US-10-724-225-2  
; Sequence 2, Application US/10724225  
; Publication No. US20040209834A1  
; GENERAL INFORMATION:  
; APPLICANT: TOCQUE, Bruno  
; WASLYK, Bohdan  
; DUBS-POTERSZMAN,  
; Marie-Christine  
; TITLE OF INVENTION: ANTAGONISTS OF THE ONCOGENIC ACTIVITY OF  
; THE PROTEIN MDW2, AND USE THEREOF IN THE TREATMENT OF  
; CANCERS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rhone-Poulenc Rorer Inc.  
; STREET: 500 Arcola Road, Mailstop 3C43  
; CITY: Collegeville

STATE: PA  
COUNTRY: USA  
ZIP: 19426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/724,225  
FILING DATE: 01-Dec-2003  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/029,327  
FILING DATE: <Unknown>  
APPLICATION NUMBER: FR 96/01340  
FILING DATE: 02-SEP-1996  
APPLICATION NUMBER: WO FR95/10331  
FILING DATE: 04-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Fehner Esq., Paul F.  
REGISTRATION NUMBER: 35,135  
REFERENCE/DOCKET NUMBER: ST95050-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 454-3839  
TELEFAX: (610) 454-3808  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 491 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-724-225-2

Query Match 98.2%; Score 545; DB 17; Length 491;  
Best Local Similarity 98.2%; Pred. No. 2.9e-55;  
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLYYLGOYIMTKRLYDEKQOHIVH 60  
DB 17 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLYYLGOYIMTKRLYDEKQOHIVY 76  
QY 61 CSNDLLGDLFGVPSPSVKEHRKIYTMIRNLLVNVNQESSDSTSVSEN 109  
DB 77 CSNDLLGDLFGVPSPSVKEHRKIYTMIRNLLVNVNQESSDSTSVSEN 125

RESULT 9  
US-10-489-802-8  
Sequence 8, Application US/10489802  
Publication No. US20040248198A1  
GENERAL INFORMATION:  
APPLICANT: St. Jude Children's Research Hospital, Inc.  
APPLICANT: Kriwacki, Richard  
APPLICANT: Bothner, Brian  
APPLICANT: Lewis, William  
TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and  
FILE REFERENCE: 44158/243642  
CURRENT APPLICATION NUMBER: US/10/489,802  
PRIOR FILING DATE: 2004-03-16  
PRIOR APPLICATION NUMBER: US 09/956,425  
PRIOR FILING DATE: 2001-09-19  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 491  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-489-802-8  
Query Match 98.2%; Score 545; DB 17; Length 491;

Best Local Similarity 98.2%; Pred. No. 2.9e-55;  
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLYYLGOYIMTKRLYDEKQOHIVH 60  
DB 17 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLYYLGOYIMTKRLYDEKQOHIVY 76  
QY 61 CSNDLLGDLFGVPSPSVKEHRKIYTMIRNLLVNVNQESSDSTSVSEN 109  
DB 77 CSNDLLGDLFGVPSPSVKEHRKIYTMIRNLLVNVNQESSDSTSVSEN 125  
RESULT 10  
US-10-723-860-2236  
Sequence 2236, Application US/10723860  
Publication No. US20040253606A1  
GENERAL INFORMATION:  
APPLICANT: Aziz, Natasha  
APPLICANT: Ginsburg, Wendy M.  
APPLICANT: Zlotnik, Albert  
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &  
FILE REFERENCE: 05882.0193.NPUS01  
CURRENT APPLICATION NUMBER: US/10/723,860  
PRIOR FILING DATE: 2003-11-26  
PRIOR APPLICATION NUMBER: 60/429,739  
PRIOR FILING DATE: 2002-11-26  
NUMBER OF SEQ ID NOS: 8393  
SOFTWARE: Patent in version 3.2  
SEQ ID NO 2236  
LENGTH: 491  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-723-860-2236

Query Match 98.2%; Score 545; DB 17; Length 491;  
Best Local Similarity 98.2%; Pred. No. 2.9e-55;  
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLYYLGOYIMTKRLYDEKQOHIVH 60  
DB 17 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLYYLGOYIMTKRLYDEKQOHIVY 76  
QY 61 CSNDLLGDLFGVPSPSVKEHRKIYTMIRNLLVNVNQESSDSTSVSEN 109  
DB 77 CSNDLLGDLFGVPSPSVKEHRKIYTMIRNLLVNVNQESSDSTSVSEN 125

RESULT 11  
US-10-057-510-4  
Sequence 4, Application US/10057510  
Publication No. US20020098580A1  
GENERAL INFORMATION:  
APPLICANT: Nandabalan, Krishnan  
APPLICANT: Yang, Meijia  
APPLICANT: Schulz, Vincent  
APPLICANT: Curagen Corporation  
TITLE OF INVENTION: MDN INTERACTING PROTEIN AND METHODS OF USE THEREOF  
FILE REFERENCE: 15966-524 MDN US  
CURRENT APPLICATION NUMBER: US/10/057,510  
CURRENT FILING DATE: 2002-01-25  
PRIOR APPLICATION NUMBER: USSN 09/510,252  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: USSN 60/121,192  
PRIOR FILING DATE: 1999-02-23  
PRIOR APPLICATION NUMBER: USSN 60/122,643  
PRIOR FILING DATE: 1999-03-03  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: Patent in Ver. 2.0  
SEQ ID NO 4  
LENGTH: 216  
TYPE: PRT  
ORGANISM: Homo sapiens



RESULT 12

US-10-287-226-380

Sequence 380, Application US/10287226

Publication No. US2004008675A1

GENERAL INFORMATION:

APPLICANT: Agee, Michele L.,

APPLICANT: Alsbrook, John P.,

APPLICANT: Bergins, Constance,

APPLICANT: Boldog, Ferenc,

APPLICANT: Burgess, Catherine E.,

APPLICANT: Chant, John S.,

APPLICANT: Chaudhuri, Amitabha,

APPLICANT: DiPippo, Vincent A.,

APPLICANT: Edinger, Shlomit R.,

APPLICANT: Eisen, Andrew,

APPLICANT: Ellerman, Karen,

APPLICANT: Galligoli, Esha A.,

APPLICANT: Gorman, Linda,

APPLICANT: Gerlach, Valerie,

APPLICANT: Ji, Weizhen,

APPLICANT: Kekuda, Ramesh,

APPLICANT: Khrantsov, Nikolai,

APPLICANT: Li, Li,

APPLICANT: Malyankar, Uriel M.,

APPLICANT: Macbougali, John R.,

APPLICANT: Mezes, Peter S.

APPLICANT: Miller, Charles E.,

APPLICANT: Millet, Isabelle,

APPLICANT: Ooi, Chean Eng,

APPLICANT: Ort, Tatiana,

APPLICANT: Padigaru, Muralidhara,

APPLICANT: Padurajan, Meera,

APPLICANT: Rastelli, Luca,

APPLICANT: Rieger, Daniel K.,

APPLICANT: Rothenberg, Mark E.,

APPLICANT: Shenoy, Suresh G.,

APPLICANT: Spaderna, Steven K.,

APPLICANT: Spytek, Kimberley A.,

APPLICANT: Taupier, Jr., Raymond J.,

APPLICANT: Vernet, Corine A.M.,

APPLICANT: Zerhusen, Bryan D.,

APPLICANT: Zhong, Wei

TITLE OF INVENTION: NOVEL PROTEINS AND

FILE REFERENCE: 21402-480C

CURRENT APPLICATION NUMBER: US/10/287

CURRENT FILING DATE: 2002-11-04

PRIOR APPLICATION NUMBER: 60/334,421

PRIOR FILING DATE: 2001-11-30

PRIOR APPLICATION NUMBER: 60/354,392

PRIOR FILING DATE: 2002-02-04

PRIOR APPLICATION NUMBER: 60/360,148

PRIOR FILING DATE: 2002-02-27

PRIOR APPLICATION NUMBER: 60/364,000

PRIOR FILING DATE: 2002-03-13

PRIOR APPLICATION NUMBER: 60/404,821

PRIOR FILING DATE: 2002-08-20

PRIOR APPLICATION NUMBER: 60/334,526

PRIOR FILING DATE: 2001-11-30

RESULT 13  
US-10-287-226-382  
US-382, Application US/10287226  
; Publication No. US2004008675A1  
; GENERAL INFORMATION:  
; APPLICANT: Agee, Michele L.,  
; APPLICANT: Alsobrook, John P.,  
; APPLICANT: Bergins, Constance,  
; APPLICANT: Boldog, Ferenc,  
; APPLICANT: Burgess, Catherine E.,  
; APPLICANT: Chant, John S.,  
; APPLICANT: Chaudhuri, Amitabha,  
; APPLICANT: DiPippo, Vincent A.,  
; APPLICANT: Edinger, Shlomit R.,  
; APPLICANT: Elsen, Andrew,  
; APPLICANT: Ellerman, Karen,  
; APPLICANT: Gangolli, Esha A.,  
; APPLICANT: Gorman, Linda,  
; APPLICANT: Gerlach, Valerie,  
; APPLICANT: Ji, WeiZhen,  
; APPLICANT: Khutuda, Ramesh,  
; APPLICANT: Khrantsov, Nikolai,  
; APPLICANT: Li, Li,  
; APPLICANT: Malyankar, Uriel M.,  
; APPLICANT: McDougall, John R.,  
; APPLICANT: Mezes, Peter S.,  
; APPLICANT: Miller, Charles E.,  
; APPLICANT: Millet, Isabelle,  
; APPLICANT: Mui, Chean Eng,  
; APPLICANT: Ott, Tatiana,  
; APPLICANT: Padiguru, Muralidhara,  
; APPLICANT: Patturajan, Meera,  
; APPLICANT: Rastelli, Luca,  
; APPLICANT: Rieger, Daniel K.,  
; APPLICANT: Rothenberg, Mark E.,  
; APPLICANT: Shenoy, Suresh G.,  
; APPLICANT: Spaderna, Steven K.,  
; APPLICANT: Szybak, Kimberley A.,  
; APPLICANT: Taupier, Jr., Raymond J.

; APPLICANT: Vernet, Corine A.M.,  
 ; APPLICANT: Zerhusen, Bryan D.,  
 ; APPLICANT: Zhong, Mei  
 ; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
 ; FILE REFERENCE: 21402-480C  
 ; CURRENT APPLICATION NUMBER: US/10/287,226  
 ; CURRENT FILING DATE: 2002-11-04  
 ; PRIOR APPLICATION NUMBER: 60/334,421  
 ; PRIOR FILING DATE: 2001-11-30  
 ; PRIOR APPLICATION NUMBER: 60/354,392  
 ; PRIOR FILING DATE: 2002-02-04  
 ; PRIOR APPLICATION NUMBER: 60/360,148  
 ; PRIOR FILING DATE: 2002-02-27  
 ; PRIOR APPLICATION NUMBER: 60/364,000  
 ; PRIOR FILING DATE: 2002-03-13  
 ; PRIOR APPLICATION NUMBER: 60/404,821  
 ; PRIOR FILING DATE: 2002-08-20  
 ; PRIOR APPLICATION NUMBER: 60/334,526  
 ; PRIOR FILING DATE: 2001-11-30  
 ; PRIOR APPLICATION NUMBER: 60/354,409  
 ; PRIOR FILING DATE: 2002-02-04  
 ; PRIOR APPLICATION NUMBER: 60/364,227  
 ; PRIOR FILING DATE: 2002-03-13  
 ; PRIOR APPLICATION NUMBER: 60/334,027  
 ; PRIOR FILING DATE: 2001-11-28  
 ; PRIOR APPLICATION NUMBER: 60/331,641  
 ; PRIOR FILING DATE: 2001-11-20  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 673  
 ; SOFTWARE: CurSeqList version 0.1  
 ; SEQ ID NO 382  
 ; LENGTH: 522  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-287-226-382

Query Match 93.6%; Score 519.5; DB 15; Length 522;  
 Best Local Similarity 76.4%; Pred. No. 3.1e-52;  
 Matches 107; Conservative 2; Mismatches 0; Indels 31; Gaps 1;  
 QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKE----- 36  
 Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKE----- 76  
 QY 37 -----VLVYLGQVIMTKRLYDEKQOHVHCSNDLLGLFGVPSFVKHEHRIYTMIVR 89  
 Db 77 PKVLDLQVLFYLGQVIMTKRLYDEKQOHVHCSNDLLGLFGVPSFVKHEHRIYTMIVR 136  
 QY 90 NLVVVNQESSDGTGSVSEN 109  
 Db 137 NLVVVNQESSDGTGSVSEN 156

RESULT 14  
 US-09-956-425-6  
 ; Sequence 6, Application US/09956425  
 ; Patent No. US20020045192A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kriwacki, Richard  
 ; APPLICANT: Bothner, Brian  
 ; APPLICANT: Lewis, William  
 ; TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and Method of Use Thereof  
 ; FILE REFERENCE: 13401/035  
 ; CURRENT APPLICATION NUMBER: US/09/956,425  
 ; CURRENT FILING DATE: 2001-09-19  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 6  
 ; LENGTH: 489  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-09-956-425-6

Query Match 87.5%; Score 485.5; DB 9; Length 489;  
 Best Local Similarity 86.2%; Pred. No. 2.9e-48;  
 Matches 94; Conservative 9; Mismatches 3; Indels 3; Gaps 1;  
 QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYLGYQYIMTKRLYDEKQOHVH 60  
 Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQNDYTMKEIIFIGYIMTKRLYDEKQOHVY 76  
 QY 61 CSNDLLGLFGVPSFVKHEHRIYTMIVRNLVVNQESSDGTGSVSEN 109  
 Db 77 CSNDLLGLFGVPSFVKHEHRIYMIYRNLVAVSQ---DSGTSLS 122  
 RESULT 15  
 US-09-966-724-4  
 ; Sequence 4, Application US/09966724  
 ; Publication No. US20040170971A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: THE JOHNS HOPKINS UNIVERSITY  
 ; 720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA  
 ; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
 ; STREET: 1001 G ST., N.W.  
 ; CITY: WASHINGTON  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20001-4597  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/966,724  
 ; FILING DATE: 01-Oct-2001  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/044,619  
 ; FILING DATE: 2001-10-01  
 ; APPLICATION NUMBER: US 07/867,840  
 ; FILING DATE: 07-APR-1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: KAGAN, SARAH A.  
 ; REGISTRATION NUMBER: 32,141  
 ; REFERENCE/DOCKET NUMBER: 01107.40148  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-508-9100  
 ; TELEFAX: 202-508-9299  
 ; TELEX: 197430 BBMB UT  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 489 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
 US-09-966-724-4

Query Match 87.5%; Score 485.5; DB 11; Length 489;  
 Best Local Similarity 86.2%; Pred. No. 2.9e-48;  
 Matches 94; Conservative 9; Mismatches 3; Indels 3; Gaps 1;  
 QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYLGYQYIMTKRLYDEKQOHVH 60  
 Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQNDYTMKEIIFIGYIMTKRLYDEKQOHVY 76  
 QY 61 CSNDLLGLFGVPSFVKHEHRIYTMIVRNLVVNQESSDGTGSVSEN 109  
 Db 77 CSNDLLGLFGVPSFVKHEHRIYMIYRNLVAVSQ---DSGTSLS 122

Search completed: January 27, 2005, 18:23:06  
Job time : 70.4 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 27, 2005, 17:45:30 ; Search time 80.8 Seconds  
(without alignments)  
483.929 Million cell updates/sec

Title: US-10-822-254-12  
Perfect score: 554  
Sequence: 1 SQIPASEQETKVRPKLLK.....NLVVNQESSDGTSTSVSEN 109

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: A\_Geneseq\_23Sep04:.\*  
2: Genesep1980s:.\*  
3: Genesep1990s:.\*  
4: Genesep2000s:.\*  
5: Genesep2001s:.\*  
6: Genesep2002s:.\*  
7: Genesep2003as:.\*  
8: Genesep2003bs:.\*  
9: Genesep2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	511	92.2	284	2 AAR75494	Aar75494 Human dou
2	511	92.2	284	2 AAR75397	Aar75397 Human dou
3	511	92.2	491	2 AAR42175	Aar42175 Human MDM
4	511	92.2	491	2 AAR76696	Aar76696 Human MDM
5	511	92.2	491	2 AAR76887	Aar76887 Human MDM
6	511	92.2	491	2 AAW15463	Aaw15463 Human MDM
7	511	92.2	491	2 AAW13380	Aaw13380 Human MDM
8	511	92.2	491	2 AAW13600	Aaw13600 Murine do
9	511	92.2	491	2 AAW48241	Aaw48241 Human MDM
10	511	92.2	491	2 AAW57241	Aaw57241 Human MDM
11	511	92.2	491	2 AAW42879	Aaw42879 Amino aci
12	511	92.2	491	2 AAW42971	Aaw42971 Amino aci
13	511	92.2	491	2 AAW94304	Aaw94304 Human MDM
14	511	92.2	491	3 AAY96567	Aay96567 MDM2 onco
15	511	92.2	491	4 AAB48284	Aab48284 Human MDM
16	511	92.2	491	5 AAE22654	Aae22654 Human Rin
17	511	92.2	491	5 AAE22698	Aae22698 Human Rin
18	511	92.2	491	5 AAE25913	Aae25913 Human dou
19	511	92.2	491	5 AAO15376	Aao15376 Human Dm2
20	511	92.2	491	7 ADD21815	Add21815 Human mdm
21	511	92.2	491	7 ADE61562	Ade61562 Human Pro
22	511	92.2	491	8 ADL23893	Adl23893 Human E3
23	511	92.2	491	8 ADO52353	Ado52353 Human p53
24	511	92.2	491	8 ADF12593	Adf12593 Protein e
25	511	92.2	491	8 ADN71936	Adn71936 MDM2 prot

26	511	92.2	491	8 ADO19417	Adol19417 Human sof
27	511	92.2	1171	4 AAU32421	Aau32421 Novel hum
28	494.5	89.3	216	3 AAB08846	Aab08846 A human M
29	485.5	87.6	522	7 ADJ95152	Adj95152 Novel NOV
30	485.5	87.6	522	7 ADJ95154	Adj95154 Novel NOV
31	451.5	81.5	489	2 AAR42176	Aar42176 Murine MDM
32	451.5	81.5	489	2 AAR76697	Aar76697 Mouse MDM
33	451.5	81.5	489	2 AAW07888	Aaw07888 Murine MDM
34	451.5	81.5	489	2 AAW15464	Aaw15464 Murine MDM
35	451.5	81.5	489	2 AAW48242	Aaw48242 Mouse MDM
36	451.5	81.5	489	2 AAW57246	Aaw57246 Mouse MDM
37	451.5	81.5	489	2 AAW42997	Aaw42997 Amino aci
38	451.5	81.5	489	2 AAW42972	Aaw42972 Amino aci
39	451.5	81.5	489	2 AAW94305	Aaw94305 Mouse MDM
40	451.5	81.5	489	5 AAE25914	Aae25914 Mouse dou
41	451.5	81.5	489	5 ABB57099	Abb57099 Mouse isc
42	451.5	81.5	489	5 AAO15375	Aao15375 Mouse Dm2
43	451.5	81.5	489	7 ADD21816	Add21816 Mouse mdm
44	451.5	81.5	489	7 ADE61560	Ade61560 Rat Proce
45	329	59.4	227	2 AAR75495	Aar75495 Human dou

## ALIGNMENTS

RESULT 1  
AAR75494  
ID AAR75494 standard; protein; 284 AA.  
XX  
AC AAR75494;  
XX  
DT 02-FEB-1996 (first entry)  
XX  
DE Human double minute 2 (hdm-2) antibody-binding region fragment 1.  
XX  
KW Human double minute gene 2; hdm-2; antibody binding region; antigen;  
KW cancer; sarcoma; rhabdomyosarcoma; diagnosis; immunoassay.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Region 1..284  
FT /note= "amino acids 1-284 of hdm-2 gene product"  
XX  
PN DE4339533-A1.  
XX  
PD 14-JUN-1995.  
XX  
PF 19-NOV-1993; 93DE-04339533.  
XX  
PR 19-NOV-1993; 93DE-04339533.  
XX  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
XX  
PI Zentgraf H, Klein R, Frey M, Martens R;  
XX  
DR WPI; 1995-216248/29.  
XX  
N-PSDB; AAQ92515.  
XX  
PT Detection of human double minute gene 2 (hdm-2) antibodies - by  
PT incubation with new hdm-2 or antibody-binding hdm-2 fragments; useful in  
PT the detection of specific cancers.  
XX  
PS Claim 11; Fig 1; 12pp; German.  
XX  
CC Fragments contg. amino acids 1-284, 58-284 and 58-491 of the hdm-2 (human  
CC double minute 2) gene product are claimed. The overlapping protein  
CC fragments contain binding regions for hdm-2- specific antibodies and are  
CC useful for identifying such antibodies in a claimed immunoassay method.  
CC The presence of anti-hdm-2 antibodies is diagnostic of certain forms of  
CC cancer, e.g. rhabdomyosarcoma  
XX  
SQ Sequence 284 AA;



```

XX AC AAR76696;
XX 16-OCT-2003 (revised)
XX 01-NOV-1995 (first entry)
XX DE Human MDM2 protein.
XX KW MDM2; sarcoma; diagnostic; DNA probe.
XX OS Homo sapiens; (cell line CaCo-2).
XX PN US5420263-A.
XX PD 30-MAY-1995.
XX PF 07-APR-1993; 93US-00044619.
XX PR 07-APR-1992; 92US-00867840.
XX PR 23-JUN-1992; 92US-00903103.
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX PI Vogelstein B, Kinzler KW;
XX WPI; 1995-206312/27.
XX DR N-PSDB; AAQ94589.
XX PT New human MDM2 cDNA - used to develop prods. for use in the diagnosis and
XX treatment of tumours.
XX PS Claim 1; Col 23-26; 34pp; English.
XX CC The human MDM2 gene is genetically altered (i.e. amplified) in human
XX tumour cells. The human MDM2 protein binds to human p53 and allows the
XX cell to escape from p53-regulated growth. Detecting that the gene has
XX become amplified or detecting increased gene product expression (using
XX probes, proteins, antibodies and inhibitors) allows diagnosis and therapy
XX of cancers such as colorectal carcinoma, lung cancer and chronic
XX myelogenous leukaemia. (Updated on 16-OCT-2003 to standardise OS field)
XX SQ Sequence 491 AA;

Query Match 92.2%; Score 511; DB 2; Length 491;
Best Local Similarity 94.5%; Pred. No. 2.3e-53;
Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLQYIMTKRLYDEKQOHIVK 60
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDKLGDLFGVKSPSVKEHRKIYTMIRNLVVVNQESSDGSSTSVSEN 109
Db 77 CSNDLLGLDFGVPSFSVKEHRKIYTMIRNLVVVNQESSDGSSTSVSEN 125

RESULT 5
AAW07887
ID AAW07887 standard; protein; 491 AA.
XX AC AAW07887;
XX 25-MAR-2003 (revised)
XX 28-JAN-1997 (first entry)
XX DE Human MDM-2, involved in tumour-development.
XX KW p53; MDM-2; binding-inhibitor; identification; tumour; cancer; neoplasia;
XX antibody fusion protein; therapy.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers

```

```

PT Modified-site 166..169
FT /label= phosphorylation_site
FT /note= "potential casein kinase II phosphorylation site"
FT Binding-site 181..185
FT /label= nuclear_localisation_signal
FT Modified-site 192..195
FT /label= phosphorylation_site
FT /note= "potential casein kinase II phosphorylation site"
FT Domain 223..274
FT /label= acid_activation_domain
FT Modified-site 269..272
FT /label= phosphorylation_site
FT /note= "potential casein kinase II phosphorylation site"
FT Modified-site 290..293
FT /label= phosphorylation_site
FT /note= "potential casein kinase II phosphorylation site"
FT Domain 305..322
FT /label= metal_binding_site
FT Domain 461..478
FT /label= metal_binding_site
XX US5550023-A.
XX PN 27-AUG-1996.
XX PD 18-MAY-1994; 94US-00245500.
XX PF 07-APR-1992; 92US-00867840.
XX PR 23-JUN-1992; 92US-00903103.
XX PR 07-APR-1993; 93US-00044619.
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX PI Vogelstein B, Kinzler KW;
XX WPI; 1996-401591/40.
XX DR N-PSDB; AAR45151.
XX PT Identification of cpds. interfering with human MDM2/p53 binding - useful
XX as therapeutic agents to treat human neoplastic cells.
XX PS Claim 26; Col 25-28; 36pp; English.
XX CC AAW07887 represents human MDM-2 derived from a human colon carcinoma cell
XX line, CaCo-2, cDNA library. The MDM-2 protein is used in a method for
XX identifying compounds that interfere with the binding of p53 and MDM-2.
XX CC In binding the p53 protein, the MDM-2 protein releases a cell from p53-
XX regulated growth, allowing cancers to develop. Therefore compounds
XX identified as interfering with the binding of MDM-2 to p53 are
XX potentially useful in the treatment of human neoplastic cells. In the
XX method pref. one or both of the proteins is a fusion protein esp. with an
XX antibody or antibody fragment which aids separation and identification.
XX CC (Updated on 25-MAR-2003 to correct PF field.)
XX SQ Sequence 491 AA;

Query Match 92.2%; Score 511; DB 2; Length 491;
Best Local Similarity 94.5%; Pred. No. 2.3e-53;
Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLQYIMTKRLYDEKQOHIVK 60
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDKLGDLFGVKSPSVKEHRKIYTMIRNLVVVNQESSDGSSTSVSEN 109
Db 77 CSNDLLGLDFGVPSFSVKEHRKIYTMIRNLVVVNQESSDGSSTSVSEN 125

RESULT 6
AAW15463
ID AAW15463 standard; protein; 491 AA.
XX

```

AC AAW15463;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 18-JUN-1997 (first entry)  
 XX  
 DE Human MDM2.  
 XX  
 KW Human; MDM2 protein; antibody; detection; cancer; diagnosis;  
 KW p53-regulated growth.  
 OS Homo sapiens.  
 OS  
 PN US5618921-A.  
 PN  
 XX 08-APR-1997.  
 PD  
 XX 17-FEB-1995; 95US-00390479.  
 PF  
 XX 07-APR-1992; 92US-00867840.  
 PR 23-JUN-1992; 92US-00903103.  
 PR 07-APR-1993; 93US-00044619.  
 XX  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 PA  
 XX Vogelstein B, Kinzler KW, Burrell M, Hill DE;  
 PI  
 XX WPI; 1997-225474/20.  
 DR N-PSDB; AAT66410.  
 XX  
 XX Antibodies specific for human MDM2 protein - for diagnosis of cancer.  
 PT  
 XX Claim 1; Col 19-24; 35pp; English.  
 PS  
 XX This sequence represents the human MDM2 protein. Antibodies that  
 CC specifically bind to human MDM2 protein may be used for detecting  
 CC elevated expression of the MDM2 gene in a human tissue or body fluid  
 CC sample, esp. for cancer diagnosis. The antibodies may be used to  
 CC interfere with the binding of p53 to MDM2. Elevated levels of MDM2 appear  
 CC to sequester p53 and allow the cell to escape from p53-regulated growth.  
 CC (Updated on 25-MAR-2003 to correct PF field.)  
 CC  
 XX Sequence 491 AA;  
 SQ  
 Query Match 92.2%; Score 511; DB 2; Length 491;  
 Best Local Similarity 94.5%; Pred. No. 2.3e-53;  
 Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQKHIVK 60  
 Db 17 SQIPASEQETLVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQKHIVY 76  
 QY 61 CSNDKLGDLFGVKSFSVKEHRKIYTMIRNLYVNVNQESSDSGTSVSEN 109  
 Db 77 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLYVNVNQESSDSGTSVSEN 125  
 RESULT 7  
 AAW13380  
 ID AAW13380 standard; protein; 491 AA.  
 XX  
 AC AAW13380;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 05-JUN-1997 (first entry)  
 XX  
 DE Human MDM2 protein.  
 XX  
 KW Human; MDM2; CaCo-2; colonic; carcinoma; probe; detection; amplification;  
 KW elevation; expression; diagnosis; neoplasia; neoplastic transformation;  
 KW sarcoma; colorectal; lung cancer; chronic myelogenous leukaemia.  
 XX  
 OS Homo sapiens.  
 OS  
 XX

PN US5606044-A.  
 XX  
 PD 25-FEB-1997.  
 XX  
 PF 17-FEB-1995; 95US-00390546.  
 XX  
 PR 07-APR-1992; 92US-00867840.  
 PR 23-JUN-1992; 92US-00903103.  
 PR 07-APR-1993; 93US-00044619.  
 XX  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 PA  
 XX Kinzler KW, Vogelstein B, Hill DE, Burrell M;  
 PI  
 XX WPI; 1997-153623/14.  
 DR N-PSDB; AAT62065.  
 XX  
 XX Detection of amplification of human MDM2 gene - useful for diagnosis of  
 PT neoplasia or potential neoplastic transformation.  
 XX  
 PS Example 1; Col 21-24; 35pp; English.  
 XX  
 CC The present sequence is the human MDM2 protein, the cDNA for which was  
 CC isolated from a human CaCo-2 colonic carcinoma cell cDNA library using a  
 CC murine MDM2 cDNA probe. The MDM2 cDNA can be used as a probe to detect  
 CC the amplification or elevated expression of a human MDM2 gene, which is  
 CC diagnostic of neoplasia or the potential for neoplastic transformation,  
 CC useful for the detection of, e.g. sarcomas, colorectal carcinoma, lung  
 CC cancer and chronic myelogenous leukaemia. (Updated on 25-MAR-2003 to  
 CC correct PF field.)  
 CC  
 XX Sequence 491 AA;  
 SQ  
 Query Match 92.2%; Score 511; DB 2; Length 491;  
 Best Local Similarity 94.5%; Pred. No. 2.3e-53;  
 Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQKHIVK 60  
 Db 17 SQIPASEQETLVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQKHIVY 76  
 QY 61 CSNDKLGDLFGVKSFSVKEHRKIYTMIRNLYVNVNQESSDSGTSVSEN 109  
 Db 77 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLYVNVNQESSDSGTSVSEN 125  
 RESULT 8  
 AAW13600  
 ID AAW13600 standard; protein; 491 AA.  
 XX  
 AC AAW13600;  
 XX  
 DT 16-JAN-1998 (first entry)  
 DT  
 XX Murine double minute 2 protein sequence.  
 DE  
 XX Mouse; Mdm2; murine double minute; phosphoprotein; binding; modulation;  
 KW tumour suppressor; p53; oncogene; cell cycle arrest; p107; antagonist;  
 KW inhibition; transcription factor; adenocarcinoma; colon; cancer; breast;  
 KW lung; stomach; myeloid leukaemia; lymphoma; hyperproliferative;  
 KW restenosis.  
 XX  
 OS Mus musculus.  
 OS  
 XX WO9709343-A2.  
 PN  
 XX 13-MAR-1997.  
 PD  
 XX 02-SEP-1996; 96WO-FR001340.  
 XX  
 XX 04-SEP-1995; 95FR-00010331.  
 XX  
 XX (RHON ) RHONE POULENC RORER SA.



PA (INRM ) INST NAT SANTE & RECH MEDICALE.  
 XX Toccoque B, Dubs-Poterszman M, Wasyluk B;  
 XX WPI; 1997-192837/17.  
 DR N-PSDB; AAT61637.  
 XX  
 PT Treating cancer with antagonist of oncogenic activity of protein Mdm2 -  
 PT or nucleic acid encoding an antagonist, also viral vectors contg. this  
 PT nucleic acid.  
 XX  
 PS Claim 2; Page 26-30; 43pp; French.  
 XX  
 CC This is the amino acid sequence of the mouse Mdm2 (murine double minute-  
 CC 2) protein, a 90 kD phosphoprotein which binds and modulates the activity  
 CC of the tumour suppressor protein p53. It has now been shown that the mdm2  
 CC protein itself has oncogenic properties, especially in a p53-null  
 CC background. Mdm2 is observed to unblock cell cycle arrest in G1 caused by  
 CC over-expression of the p107 protein. This is especially done by the  
 CC region covering amino acid 1-134. The invention therefore relates to  
 CC antagonists able to inhibit the oncogenic activity of mdm2. These include  
 CC fragments of the p53 protein, especially amino acids 1-52, 1-41, 6-41, 16  
 CC -25 or 18-23 (AAW13602-6), or fragments of transcription factors e.g.  
 CC TFII, TBP or TAF250, which bind amino acids 1-134 of mdm2. Other  
 CC inhibitors include compounds which disrupt binding to region 135-491 of  
 CC mdm2, e.g. Rb, L5 or the transcription factor E2F. The antagonists are  
 CC used to treat e.g. adenocarcinoma of the colon; cancer of the breast,  
 CC lung or stomach; myeloid leukaemia; B cell lymphoma, or other  
 CC hyperproliferative conditions such as restenosis  
 XX  
 XX Sequence 491 AA;  
 SQ

Query Match 92.2%; Score 511; DB 2; Length 491;  
 Best Local Similarity 94.5%; Pred. No. 2.3e-53;  
 Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 SQIPASEQETKVRPKPLKLLKLLKSVGAQKDTYTMKEVLHYLQYIMTKRLYDEKQOHIVK 60  
 Db 17 SQIPASEQETLVRPKPLKLLKLLKSVGAQKDTYTMKEVLHYLQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDKLGDLFGVKFSVKEHRKIYTMIRNVLVNVNQSSDSGTSVSEN 109  
 Db 77 CSNDLLGDLFGVPSFVKEHRKIYTMIRNVLVNVNQSSDSGTSVSEN 125

RESULT 9  
 AAW48241  
 ID AAW48241 standard; protein; 491 AA.  
 XX  
 AC AAW48241;  
 XX  
 DT 18-JUN-1998 (first entry)  
 XX  
 DE Human MDM2.  
 XX  
 KW Human; MDM2; hMDM2; tumour; cancer; diagnosis; neoplastic disease;  
 KW sarcoma; liposarcoma; malignant fibrous histiocytoma; osteosarcoma.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US5736338-A.  
 XX  
 PD 07-APR-1998.  
 XX  
 PF 17-FEB-1995; 95US-00390517.  
 XX  
 PR 07-APR-1992; 92US-00867840.  
 XX  
 PR 23-JUN-1992; 92US-00903103.  
 XX  
 PR 07-APR-1993; 93US-00044619.  
 XX  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 PI Vogelstein B, Kinzler KW, Hill DE, Burrell M;  
 XX  
 OS Homo sapiens.  
 XX  
 PN US5736338-A.  
 XX  
 PD 07-APR-1998.  
 XX  
 PF 17-FEB-1995; 95US-00390517.  
 XX  
 PR 07-APR-1992; 92US-00867840.  
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 PR 23-JUN-1992; 92US-00903103.  
 XX  
 PR 07-APR-1993; 93US-00044619.  
 XX  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 PI Vogelstein B, Kinzler KW, Hill DE, Burrell M;

Query Match 92.2%; Score 511; DB 2; Length 491;  
 Best Local Similarity 94.5%; Pred. No. 2.3e-53;  
 Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 SQIPASEQETKVRPKPLKLLKLLKSVGAQKDTYTMKEVLHYLQYIMTKRLYDEKQOHIVK 60  
 Db 17 SQIPASEQETLVRPKPLKLLKLLKSVGAQKDTYTMKEVLHYLQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDKLGDLFGVKFSVKEHRKIYTMIRNVLVNVNQSSDSGTSVSEN 109  
 Db 77 CSNDLLGDLFGVPSFVKEHRKIYTMIRNVLVNVNQSSDSGTSVSEN 125

RESULT 10  
 AAW57241  
 ID AAW57241 standard; protein; 491 AA.  
 XX  
 AC AAW57241;  
 XX  
 DT 10-AUG-1998 (first entry)  
 XX  
 DE Human MDM2 protein.  
 XX  
 KW Human; p53; MDM2; tumour; growth inhibition; amplification;  
 KW malignant fibrous histiocytoma; liposarcoma.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US5756455-A.  
 XX  
 PD 26-MAY-1998.  
 XX  
 PF 17-FEB-1995; 95US-00390515.  
 XX  
 PR 07-APR-1992; 92US-00867840.  
 XX  
 PR 23-JUN-1992; 92US-00903103.  
 XX  
 PR 07-APR-1993; 93US-00044619.  
 XX  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 PI Vogelstein B, Kinzler KW;  
 XX  
 DR WPI; 1998-321574/28.  
 XX  
 DR N-PSDB; AAV28876.  
 XX  
 PT Inhibiting growth of tumour cells having MDM2 gene amplification - with  
 PT p53 protein fragment.  
 XX  
 PS Claim 1; Col 23-28; 40pp; English.  
 XX  
 CC A method has been developed for inhibiting the growth of tumour cells  
 CC containing a human MDM2 gene amplification. The method comprises treating  
 CC the tumour cells with a DNA molecule that expresses a polypeptide capable  
 CC of binding to human MDM2 protein. The present sequence represents human  
 CC MDM2 protein. The present invention describes three preferred  
 CC polypeptides for binding human MDM2: (1) the polypeptide comprises amino

XX WPI; 1998-239206/21.  
 DR N-PSDB; AAV20549.  
 XX  
 PT Cancer diagnosis - by determination of MDM2 protein.  
 XX  
 PS Claim 1; Col 25-28; 35pp; English.  
 XX  
 CC The present sequence represents human MDM2 (hMDM2) which is used in the  
 CC method of the present invention. The present invention describes a method  
 CC for diagnosing a neoplastic disease caused by overexpression of MDM2  
 CC protein. The method comprises detecting an elevated cellular amount of  
 CC this protein. The method is useful for the diagnosis of sarcoma,  
 CC especially liposarcoma, malignant fibrous histiocytoma or osteosarcoma  
 XX  
 SQ Sequence 491 AA;  
 Query Match 92.2%; Score 511; DB 2; Length 491;  
 Best Local Similarity 94.5%; Pred. No. 2.3e-53;  
 Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 SQIPASEQETKVRPKPLKLLKLLKSVGAQKDTYTMKEVLHYLQYIMTKRLYDEKQOHIVK 60  
 Db 17 SQIPASEQETLVRPKPLKLLKLLKSVGAQKDTYTMKEVLHYLQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDKLGDLFGVKFSVKEHRKIYTMIRNVLVNVNQSSDSGTSVSEN 109  
 Db 77 CSNDLLGDLFGVPSFVKEHRKIYTMIRNVLVNVNQSSDSGTSVSEN 125

CC acids 1-50 of p53 (see AAW57240) ; (2) the polypeptide comprises amino  
 CC acids 13-41 of p53 (see AAW57240) and at least none additional p53  
 CC residues on the N- or C-terminal side, provided that the polypeptide  
 CC lacks the homooligomerisation domain of p53; (3) the polypeptide  
 CC comprises amino acids 13-41 of p53 (see AAW57241) and at least nine  
 CC additional p53 residues on the N- or C-terminal side, provided that the  
 CC polypeptide lacks amino acids 138-393 of p53. Some malignant fibrous  
 CC histiocytomas and liposarcomas have an MDM2 gene amplification, so  
 CC detection of increased expression of MDM2 gene products indicates  
 CC tumourigenesis  
 XX  
 SQ Sequence 491 AA;  
 Query Match 92.2%; Score 511; DB 2; Length 491;  
 Best Local Similarity 94.5%; Pred. No. 2.3e-53;  
 Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIVK 60  
 DB 17 SQIPASEQETLVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIVY 76  
 QY 61 CSNDKLGDLFGVKSPFVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 109  
 DB 77 CSNDLLGDLFGVPFVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 125  
 RESULT 11  
 ID AAW42879  
 AC AAW42879 standard; protein; 491 AA.  
 AC AAW42879;  
 DT 30-APR-1998 (first entry)  
 DE Amino acid sequence of human MDM2.  
 KW MDM2; tumour; diagnosis; neoplasia; DNA binding protein; p53 polypeptide;  
 KW binding; tumour cell; p53-regulated growth; inhibition;  
 KW anti-cancer agent.  
 OS Homo sapiens.  
 XX US5708136-A.  
 XX 13-JAN-1998.  
 XX 17-FEB-1995; 95US-00390516.  
 XX 07-APR-1992; 92US-00867840.  
 XX 23-JUN-1992; 92US-00903103.  
 XX 07-APR-1993; 93US-00044619.  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 XX Vogelstein B, Kinzler KW, Burrell M, Hill DE;  
 XX WPI; 1998-100408/09.  
 XX Human MDM2 binding polypeptide - comprises fragments of p53, useful in re  
 XX -establishing p53-regulated growth control in cells over-expressing MDM2.  
 XX Disclosure; Col 23-28; 41pp; English.  
 XX The present sequence represents human MDM2. The MDM2 gene is amplified in  
 XX some human tumours. The amplification of this gene is diagnostic of  
 XX neoplasia or its potential. It is speculated that the MDM2 protein is a  
 XX potential DNA binding protein that functions in the modulation of  
 XX expression of other genes and, when present in excess, interferes with  
 XX normal constraints on cell growth. A cell containing three recombinant  
 XX DNA constructs was produced. These constructs encode an MDM2 protein  
 XX fused to a sequence-specific DNA binding domain, a p53 polypeptide fused  
 XX to a transcriptional activation domain, and a reporter gene downstream  
 XX from a DNA element which is recognised by the sequence-specific DNA-  
 XX binding domain. The cell is used to identify a compound which interferes  
 XX with the binding of MDM2 and p53. Since MDM2 is overexpressed in tumour

CC binding domain. The cell is used to identify a compound which interferes  
 CC with the binding of MDM2 and p53. Since MDM2 is overexpressed in tumour  
 CC cells and since binding of MDM2 to p53 appears to allow tumour cells to  
 CC escape from p53-regulated growth, compounds that inhibit such binding  
 CC would be useful as anti-cancer agents  
 XX  
 SQ Sequence 491 AA;  
 Query Match 92.2%; Score 511; DB 2; Length 491;  
 Best Local Similarity 94.5%; Pred. No. 2.3e-53;  
 Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIVK 60  
 DB 17 SQIPASEQETLVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIVY 76  
 QY 61 CSNDKLGDLFGVKSPFVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 109  
 DB 77 CSNDLLGDLFGVPFVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 125  
 RESULT 12  
 ID AAW42971  
 AC AAW42971 standard; protein; 491 AA.  
 AC AAW42971;  
 DT 29-APR-1998 (first entry)  
 DE Amino acid sequence of human MDM2.  
 KW MDM2; tumour; diagnosis; neoplasia; DNA binding protein; p53 polypeptide;  
 KW binding; tumour cell; p53-regulated growth; inhibition;  
 KW anti-cancer agent.  
 OS Homo sapiens.  
 XX US5702903-A.  
 XX 30-DEC-1997.  
 XX 13-NOV-1995; 95US-00557393.  
 XX 07-APR-1992; 92US-00867840.  
 XX 23-JUN-1992; 92US-00903103.  
 XX 07-APR-1993; 93US-00044619.  
 XX 18-MAY-1994; 94US-00245500.  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 XX Vogelstein B, Kinzler KW;  
 XX WPI; 1998-076411/07.  
 XX N-PSDB; AAV03607.  
 XX Cell containing reporter construct containing human MDM2 and p53 genes -  
 XX for identifying compounds that interfere with binding of human MDM2 to  
 XX human p53, useful as anti-cancer agents.  
 XX Disclosure; Coulmans 22-28; 37pp; English.  
 XX The present sequence represents human MDM2. The MDM2 gene is amplified in  
 XX some human tumours. The amplification of this gene is diagnostic of  
 XX neoplasia or its potential. It is speculated that the MDM2 protein is a  
 XX potential DNA binding protein that functions in the modulation of  
 XX expression of other genes and, when present in excess, interferes with  
 XX normal constraints on cell growth. A cell containing three recombinant  
 XX DNA constructs was produced. These constructs encode an MDM2 protein  
 XX fused to a sequence-specific DNA binding domain, a p53 polypeptide fused  
 XX to a transcriptional activation domain, and a reporter gene downstream  
 XX from a DNA element which is recognised by the sequence-specific DNA-  
 XX binding domain. The cell is used to identify a compound which interferes  
 XX with the binding of MDM2 and p53. Since MDM2 is overexpressed in tumour

CC cells and since binding of MDM2 to p53 appears to allow tumour cells to  
 CC escape from p53-regulated growth, compounds that inhibit such binding  
 CC would be useful as anti-cancer agents

SX Sequence 491 AA;

Query Match 92.2%; Score 511; DB 2; Length 491;  
 Best Local Similarity 94.5%; Pred. No. 2.3e-53;  
 Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDYTTMKEVLHYLGQYIMTKRLYDEKQOHIVK 60  
 DB 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDYTTMKEVLHYLGQYIMTKRLYDEKQOHIVY 76  
 QY 61 CSNDKLGDLFGVKFSVKEHRKIYTMIRNVLVNVNQSSDSGTSVSEN 109  
 DB 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNVLVNVNQSSDSGTSVSEN 125

#### RESULT 13

AAW94304  
 ID AAW94304 standard; protein; 491 AA.

AC AAW94304;

DT 13-APR-1999 (first entry)

DE Human MDM2.

KW Human; MDM2; p53; tumorigenesis; growth regulation; diagnosis;  
 KW malignant fibrous histiocytoma; MFH; liposarcoma.

OS Homo sapiens.

PN US5858976-A.

PD 12-JAN-1999.

PF 14-FEB-1997; 97US-00801718.

PR 07-APR-1992; 92US-00867840.

PR 23-JUN-1992; 92US-00903103.

PR 07-APR-1993; 93US-00044619.

PR 17-FEB-1995; 95US-00390515.

PA (UWJO ) UNIV JOHNS HOPKINS.

PI Kinzler KW, Vogelstein B;

DR WPI; 1999-152105/13.

DR N-PSDB; AAX03947.

PT Inhibiting growth of tumour cells having MDM2 gene amplification - with

PS MDM2-binding p53 fragment.

Claim 1; Col 23-28; 41pp; English.

The present invention describes: (1) a method for inhibiting the growth  
 of tumour cells which contain a human MDM2 gene amplification, comprising  
 administering to the cells a DNA molecule that expresses a polypeptide  
 consisting of a portion of p53 i.e. amino acids 13-41 of the 64 amino  
 acid sequence given in AAW94303, the polypeptide being capable of binding  
 to human MDM2 (the present sequence); (2) a method as in (1) where the  
 polypeptide lacks the homo-oligomerisation domain of p53; and (3) a  
 method as in (1) where the polypeptide lacks amino acids 138-393 of p53.  
 The method is useful for treating the following tumour types which have a  
 MDM2 gene amplification: M-7 malignant fibrous histiocytoma (MFH), M-20  
 MFH, L-9 liposarcoma, KL7 liposarcoma, KL28 liposarcoma, KL30  
 liposarcoma, and OSA-CL MFH

SX Sequence 491 AA;

Query Match 92.2%; Score 511; DB 2; Length 491;

Best Local Similarity 94.5%; Pred. No. 2.3e-53;  
 Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDYTTMKEVLHYLGQYIMTKRLYDEKQOHIVK 60  
 DB 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDYTTMKEVLHYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDKLGDLFGVKFSVKEHRKIYTMIRNVLVNVNQSSDSGTSVSEN 109  
 DB 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNVLVNVNQSSDSGTSVSEN 125

#### RESULT 14

AAI96567

ID AAI96567 standard; protein; 491 AA.

AC AAI96567;

DT 12-SEP-2000 (first entry)

DE MDM2 oncoprotein.

KW hEST2; telomerase; catalytic subunit; reverse transcriptase; life-span;  
 KW retinoblastoma; p53; tumour suppressor; inhibitor; arteriosclerosis;  
 KW proliferation; immortal; tumour therapy; macular degeneration; activator;  
 KW INK4; MDM2; oncoprotein.

OS Homo sapiens.

PN WO200031238-A2.

PD 02-JUN-2000.

PF 24-NOV-1999; 99WO-US027907.

PR 25-NOV-1998; 98US-0109891P.

PR 17-FEB-1999; 99US-0120549P.

PA (GENE-) GENETICA INC.

PI Hannon GJ, Beach DH;

DR WPI; 2000-400055/34.

DR N-PSDB; AAA29389.

PT New method for increasing the proliferative capacity of cell lines  
 PT comprises administering agents reversibly activating telomerase activity  
 PT and reversibly inactivating Rb/INK4 and/or p53 pathways useful in  
 PT treating age related diseases.

PS Claim 5; Page 120; 123pp; English.

The invention concerns methods and reagents for extending the life-span,  
 e.g. the number of mitotic divisions, of a cell. The method relies on  
 activation of a telomerase activity and inhibition of one or both of a  
 retinoblastoma (Rb)/INK4 pathway or a p53 pathway. Phosphorylation of Rb  
 by cyclin-dependent kinases, cdk4 and cdk6, releases the cells into the  
 division cycle. Binding of INK4 family members, e.g. the tumour  
 suppressor p16INK4a, inhibits kinase activity and results in growth  
 arrest. Rb inactivators can selectively and reversibly inactivate an  
 Rb/INK4 pathway, especially an Rb/p16INK4a pathway. The oncoprotein MDM2  
 is a cellular inhibitor of Rb/E2F function and the p53 tumour suppressor  
 and can also be used in the methods. Other molecules which can be used  
 include cdk4 or cdk6 mutants. In particular, a cdk4 mutant is one which  
 differs from at one or more of residues K22, R24, H95 and/or D97.  
 Additional constructs include a papilloma virus E7 protein, or other  
 viral oncoprotein which bypasses Rb and/or p53. Antisense constructs of  
 the Rb and p16INK4a genes may also be used. The methods are useful for  
 increasing the proliferative capacity of cells. The cells are  
 subsequently of use in pharmaceutical and cosmetic preparations used to  
 treat conditions related to (premature) ageing, e.g. macular degeneration  
 and arteriosclerosis. The cells can also be used to replace tumour cell  
 lines in vitro and for studies on biochemical and physiological aspects

CC of growth and differentiation. Long lived (immortal) cells could also be  
CC of use in the production of normal or genetically engineered  
CC biotechnology products  
XX SQ Sequence 491 AA;

Query Match 92.2%; Score 511; DB 3; Length 491;  
Best Local Similarity 94.5%; Pred. No. 2.3e-53;  
Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 SQIPASEQETKVRPKPLKLLKLSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIVY 60  
Db 17 SQIPASEQETLVRPKPLKLLKLSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDKLGDLFGVKSFSVKEHRKIYTMIRNLVVVNQOESSDSGTSVSEN 109  
Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVVNQOESSDSGTSVSEN 125

Search completed: January 27, 2005, 18:06:16  
Job time : 80.8 secs

RESULT 15  
AAB48284  
ID AAB48284 standard; protein; 491 AA.  
XX AC AAB48284;  
XX DT 02-APR-2001 (first entry)  
XX DE Human MDM2 protein.  
XX KW S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; ZF;  
XX KW CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;  
XX KW Bad; Bcl-2; tumour; cytostatic.  
XX OS Homo sapiens.  
XX PN WO200075184-A1.  
XX PD 14-DEC-2000.  
XX PF 05-JUN-2000; 2000WO-US015449.  
XX PR 04-JUN-1999; 99US-0137494P.  
XX PA (UYVA ) UNIV YALE.  
XX PI Zhang H, Tsvetkov LM, Kondo T;  
XX DR WPI; 2001-061703/07.  
XX DR N-PSDB; AAC84596.  
XX PT Modulating polypeptide levels in a cell, diagnosing and treating tumor,  
XX PT involves altering levels of proteins such as S-phase kinase associated  
XX PT proteins 1, 2 and cullin/CDC53 proteins.  
XX PS Claim 5; Page 93-95; 162pp; English.  
XX CC The invention relates to methods of altering the polypeptide levels in a  
XX CC cell, using proteins selected from S-phase kinase associated proteins 1  
XX CC and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the  
XX CC cullin/ CDC53 family of proteins). The method is useful for altering the  
XX CC level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2  
XX CC polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for  
XX CC detecting tumours, and in monitoring tumor treatment in a mammal. Agents  
XX CC that modulate interactions between SKP and target proteins are useful for  
XX CC treating tumours  
XX SQ Sequence 491 AA;

Query Match 92.2%; Score 511; DB 4; Length 491;  
Best Local Similarity 94.5%; Pred. No. 2.3e-53;  
Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 SQIPASEQETKVRPKPLKLLKLSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIVY 60

Db 17 SQIPASEQETLVRPKPLKLLKLSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIVY 76  
Qy 61 CSNDKLGDLFGVKSFSVKEHRKIYTMIRNLVVVNQOESSDSGTSVSEN 109  
Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVVNQOESSDSGTSVSEN 125

Search completed: January 27, 2005, 18:06:16  
Job time : 80.8 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 27, 2005, 17:52:56 ; Search time 19.8 Seconds  
(without alignments)  
529.678 Million cell updates/sec

Title: US-10-822-254-12

Perfect score: 554

Sequence: 1 SQIPASQETKVRPKPKLLK.....NLVVNQESSDSSTSVSEN 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR.79.\*

1: PIR1.\*

2: PIR2.\*

3: PIR3.\*

4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	511	92.2	491	1 S24354	p53-binding protei
2	451.5	81.5	489	2 S15349	mdm2 protein - mou
3	278.5	50.3	489	2 S71955	MDM2-like p53-bind
4	77.5	14.0	709	2 E54213	DNA topoisomerase
5	76.5	13.8	337	2 T19592	hypothetical prote
6	73	13.2	1751	2 A45604	major blood-stage
7	72	13.0	755	2 S58718	probable nuclear p
8	71.5	12.9	244	2 D71608	hypothetical prote
9	71.5	12.9	840	2 H96635	unknown protein, 7
10	71	12.8	838	2 T45557	eyeless, long form
11	70.5	12.7	223	2 C69215	conserved hypothet
12	70.5	12.7	525	2 T15185	hypothetical prote
13	70	12.6	215	2 S28062	homeotic protein g
14	70	12.6	337	1 ZHBPQ4	gene H protein - p
15	69	12.5	187	2 S70186	21K protein - Shig
16	69	12.5	206	1 XUBYWC	methylated-DNA-lpr
17	69	12.5	413	2 E83950	processing protein
18	69	12.5	1233	1 G71612	novel serine/threo
19	68.5	12.4	425	2 T50184	mammalian swi/snf
20	68.5	12.4	636	2 H96666	probable phytochro
21	68.5	12.4	882	2 S57704	hypothetical prote
22	68.5	12.4	1292	2 F64237	DNA-directed RNA p
23	68	12.3	1098	2 S38100	hypothetical prote
24	67.5	12.2	245	2 F71899	hypothetical prote
25	67.5	12.2	263	2 AB2559	transposase all806
26	67.5	12.2	319	2 A42277	traA protein - Ent
27	67.5	12.2	353	2 D69001	conserved hypothet
28	67.5	12.2	446	2 S35524	telomere-binding p
29	67.5	12.2	600	2 H81733	DNA primase TC0175

30 67 12.1 286 2 B97743  
31 67 12.1 418 2 B57511  
32 67 12.1 683 2 T38254  
33 67 12.1 685 1 SXBP74  
34 67 12.1 698 1 S31630  
35 67 12.1 698 1 S31714  
36 66.5 12.0 467 2 T25848  
37 66.5 12.0 928 1 RBHU  
38 66 11.9 146 2 G71940  
39 66 11.9 170 2 T31967  
40 66 11.9 258 2 A64000  
41 66 11.9 303 2 B95101  
42 66 11.9 303 2 C97969  
43 66 11.9 374 2 AD1970  
44 66 11.9 425 2 C97035  
45 66 11.9 456 2 AG3471

#### ALIGNMENTS

##### RESULT 1

S24354

p53-binding protein mdm2 - human

N:Alternate names: mdm-2 oncogene; mouse double minute 2 homolog; p53-associated phospho

N:Contains: p53-binding protein mdm2, splice form A

C:Species: Homo sapiens (man)

C:Date: 17-Mar-2000 #sequence revision 17-Mar-2000 #text\_change 17-Mar-2000

C:Accession: S24354; S57338; G02026

R:Oliner, J.D.; Kinzler, K.W.; Meltzer, P.S.; George, D.L.; Vogelstein, B.

Nature 358, 80-83, 1992

A:Title: Amplification of a gene encoding a p53-associated protein in human sarcomas.

A:Reference number: S24354; MUID:92310576; PMID:1614537

A:Accession: S24354

A:Molecule type: mRNA

A:Residues: 1-491 <OLI>

A:Cross-references: EMBL:Z12020; NID:g35211; PIDN:CAA78055.1; PID:g35212

R:Zauberman, A.; Flusberg, D.; Haupt, Y.; Barak, Y.; Oren, M.

Nucleic Acids Res. 23, 2584-2592, 1995

A:Title: A functional p53-responsive intronic promoter is contained within the human mdm

A:Reference number: S57338; MUID:95380270; PMID:7651818

A:Accession: S57338

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-16,'P',18-24 <ZAU>

A:Cross-references: EMBL:U28935; NID:g904033; PIDN:AAA82237.1; PID:g904034

R:Lunec, J

Submitted to the EMBL Data Library, August 1995

A:Description: Multiple alternate spliced mdm2 transcripts with loss of p53 binding doma

A:Reference number: G09070

A:Accession: G02026

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-27,223-491 <LUN>

A:Cross-references: EMBL:U33199; NID:g992676; PIDN:AAA75514.1; PID:g992677

A:Experimental source: splice form A

C:Genetics:

A:Gene: GDB:MDM2

A:Cross-references: GDB:250456; OMIM:164785

A:Map position: 12q14.3-12q15

C:Superfamily: human p53-binding protein mdm2

C:Keywords: alternative splicing; oncogene; phosphoprotein

F:1-491/Product: p53-binding protein mdm-2 #status predicted <MAT1>

F:1-27,223-491/Product: p53-binding protein mdm-2, splice form A #status predicted <MAT2>

Query Match 92.2%; Score 511; DB 1; Length 491;

Best Local Similarity 94.5%; Pred. No. 8.3e-43;

Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 SQIPASQETKVRPKPKLLKSVGAQKDTYTMKEVLHVGQYIMTKRLYDEKQOHIVK 60

Db 17 SQIPASQETLVRPKPKLLKSVGAQKDTYTMKEVLHVGQYIMTKRLYDEKQOHIVY 76

```
Qy 61 CSNDKLGDLFGVKSFSVKEHRKIYTMIRNLVVVNQSSDGSSTSVSEN 109
|||||
Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVVNQSSDGSSTSVSEN 125

RESULT 2
S15349
mdm2 protein - mouse
C:Species: Mus musculus (house mouse)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S15349
R:Fakhrazadeh, S.S.; Trusko, S.P.; George, D.L.
EMBO J. 10, 1565-1569, 1991
A:Title: Tumorigenic potential associated with enhanced expression of a gene that is amp
A:Reference number: S15349; MUID:91224107; PMID:2026149
A:Accession: S15349
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-489 <FAK>
A:Cross-references: UNIPROT:P23804; EMBL:X58876; NID:g53038; PIDN:CAA41684.1; PID:g53039
C:Genetics:
A:Gene: mdm2
C:Superfamily: human p53-binding protein mdm2

Query Match 81.5%; Score 451.5; DB 2; Length 489;
Best Local Similarity 82.6%; Pred. No. 6.3e-37;
Matches 90; Conservative 7; Mismatches 9; Indels 3; Gaps 1;

Qy 1 SQIPASEQETKVRPKPLKLLKSVGAQKQYTMKEVLHYLGYIMTKRLYDEKQOHIVK 60
|||||
Db 17 SQIPASEQETLVRPKPLKLLKSVGAQNDYTMKEIIFYIGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDKLGDLFGVKSFSVKEHRKIYTMIRNLVVVNQSSDGSSTSVSEN 109
|||||
Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVVNQSSDGSSTSVSEN 122

RESULT 3
S71955
MDM2-like p53-binding protein MDMX - mouse
C:Species: Mus musculus (house mouse)
C>Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
C:Accession: S71955
R:Shvarts, A.; Steegenga, W.T.; Riteco, N.; van Laar, T.; Dekker, P.; Bazuine, M.; van H
EMBO J. 15, 5349-5357, 1996
A:Title: MDMX: a novel p53-binding protein with some functional properties of MDM2.
A:Reference number: S71955; MUID:97050840; PMID:8895579
A:Accession: S71955
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-489 <SHV>
A:Cross-references: UNIPROT:Q35618; EMBL:AF007110; NID:g2253388; PIDN:AAB62927.1; PID:g2
C:Genetics:
A:Gene: MDMX
C:Function:
A:Description: inhibits transcription activation function of tumour suppressor protein p
C:Superfamily: human p53-binding protein mdm2

Query Match 50.3%; Score 278.5; DB 2; Length 489;
Best Local Similarity 52.4%; Pred. No. 8.2e-20;
Matches 55; Conservative 19; Mismatches 20; Indels 11; Gaps 1;

Qy 5 ASEQETKVRPKPLKLLKSVGAQKQYTMKEVLHYLGYIMTKRLYDEKQOHIVKCSND 64
|||||
Db 20 SSEQISQVRPKQLKILHAAGAQQEVFTKEVIMHYLGYIMVKQYDQOQHMYVCGD 79

Qy 65 KLGDLFGVKSFSVKEHRKIYTMIRNLVVVNQSSDGSSTSVSEN 109
|||||
Db 80 LLGDLGCGSFSVSKDPSPLYDMLRKNLV-----TSASNN 113

RESULT 4
E64213
```

```
DNA topoisomerase (EC 5.99.1.2) - Mycoplasma genitalium
N:Alternate names: type I DNA topoisomerase
C:Species: Mycoplasma genitalium
C>Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
C:Accession: E64213
R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
C.A.; Venter, J.C.
Science 270, 397-403, 1995
A:Title: The minimal gene complement of Mycoplasma genitalium.
A:Reference number: A64200; MUID:96026346; PMID:7569993
A:Accession: E64213
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-709 <TIGR>
A:Cross-references: UNIPROT:P47368; GB:U39691; GB:L43967; NID:g1045794; PID:g1045802; TI
A:Experimental source: strain G-37
C:Genetics:
A:Genetic code: SOC3
C:Superfamily: DNA topoisomerase I
C:Keywords: isomerase

Query Match 14.0%; Score 77.5; DB 2; Length 709;
Best Local Similarity 24.7%; Pred. No. 9.5;
Matches 24; Conservative 17; Mismatches 39; Indels 17; Gaps 3;

Qy 30 DTYTMKEVLHYLGO---YIMTK-----RLYDE-----KQOHIVKCSNDKLGDLFGV 72
|||||
Db 424 DAKTSRTIVAFINQKNKFTSSKLLFDGQYRLYEEIKPNTKDELYIDLSKLGDKKFSF 483

Qy 73 KSFVSKEHRKIYTMIRNLVVVNQSSDGSSTSVSEN 109
|||||
Db 484 EKISVNEHKNPPRYTQASLIELEKSNIGRPSYTN 520

RESULT 5
T19592
hypothetical protein C30H6.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T19592
R:Mortimore, B.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19148
A:Accession: T19592
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-337 <WIL>
A:Cross-references: UNIPROT:O45279; EMBL:Z81044; PIDN:CAB02813.1; GSPDB:GN00022; CESP:C3
A:Experimental source: clone C30H6
C:Genetics:
A:Gene: CESP:C30H6.7
A:Map position: 4
A:Introns: 19/2; 85/3; 120/3; 166/3; 240/2; 286/2

Query Match 13.8%; Score 76.5; DB 2; Length 337;
Best Local Similarity 26.6%; Pred. No. 5.1;
Matches 33; Conservative 17; Mismatches 33; Indels 41; Gaps 6;

Qy 14 PKPK-LLK--LLKSVGAQKQYTMKEVLHYLGYIMTKRLYDEKQOHIVKCSNDKLGDLF 70
|||||
Db 44 PKNRNILKGDYMKIVEAEK---LKPVAHH-----AHAPKETHIENKSIKKSDF 90

Qy 71 GVKFSVKEHR-----KIYTMIRNLVVVNQ-----QESDSDGTS 105
|||||
Db 91 GANNRSLRHQDIPLSNIRATIAKRLTASKQOIPEHYQGVDRIDDLALRQKLKSGTA 150

Qy 106 VSEN 109
|||
Db 151 VSLN 154

RESULT 6
```

A45604  
major blood-stage surface antigen Pv200 - Plasmodium vivax  
C:Species: Plasmodium vivax  
C>Date: 22-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C:Accession: A45604  
R:Gibson, H.L.; Tucker, J.E.; Kaelow, D.C.; Krettli, A.U.; Collins, W.E.; Kiefer, M.C.;  
Mol. Biochem. Parasitol. 50, 325-333, 1992  
A>Title: Structure and expression of the gene for Pv200, a major blood-stage surface antigen  
A:Reference number: A45604; MUID:92158013; PMID:1371329  
A:Accession: A45604  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1751 <GIB>  
A:CROSS-references: UNIPROT:Q26194; GB:M75674; NID:gl60608; PID:q457336  
A>Note: sequence extracted from NCBI backbone (NCBI:83591, NCBIP:83592)  
C:Superfamily: major merozoite surface antigen  
C:Keywords: surface antigen

Query Match 13.2%; Score 73; DB 2; Length 1751;  
Best Local Similarity 27.6%; Pred. No. 74;  
Matches 35; Conservative 20; Mismatches 42; Indels 30; Gaps 7;  
A:Map position: 141

Qy 4 PASEQETKVRPKP-----KLLKLLKSVGA-OKDTY----TWKEVLHYLGQVIMTKR 49  
Db 816 PPSPTAAVAAPAPTMSKLEYLEKLDPLKSAVACHKHIFVNTNMKKEL--LDQY----K 869

Qy 50 LYDEKQOHVRCNSNDKGLDGLFGVKS-----FSV-----KEHRKIYTYMYRNVLVVNQES 99  
Db 870 LNADQNKINETKCDLDELFFNVQNNLPAMYSIYDSMSNELQNLIELYQKEMVYNYKN 929

Qy 100 SDSGTSV 106  
Db 930 KDTDKKI 936

RESULT 7  
S58718  
probable nuclear protein YNL059c - yeast (Saccharomyces cerevisiae)  
N:Alternate names: protein N2430; protein YNL1620  
C:Species: Saccharomyces cerevisiae  
C>Date: 16-Feb-1996 #sequence\_revision 23-Feb-1996 #text\_change 09-Jul-2004  
C:Accession: S58718; S62987  
R:Bergez, P.; Doignon, F.; Crouzet, M.  
Yeast 11, 967-974, 1995  
A>Title: The sequence of a 44 420 bp fragment located on the left arm of chromosome XIV  
A:Reference number: S58711; MUID:96021608; PMID:8533472  
A:Accession: S58718  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-755 <BER>  
A:CROSS-references: UNIPROT:P53946; EMBL:U12141; NID:gl314216; PIDN:AAA99652.1; PID:g994  
A>Note: The nucleotide sequence was submitted to the EMBL Data Library, July 1994  
R:Bergez, P.; Doignon, F.; Crouzet, M.  
submitted to the Protein Sequence Database, April 1996  
A:Reference number: S62975  
A:Accession: S62987  
A:Molecule type: DNA  
A:Residues: 1-755 <BEW>  
A:CROSS-references: EMBL:L271335; NID:gl3101931; PID:e239897; PID:gl3101932; MIPS:YNL059c  
A:Experimental source: strain S288C  
C:Genetics:  
A:Gene: SGD:ARP5  
A:CROSS-references: SGD:S0005004; MIPS:YNL059c  
A:Map position: 141

Query Match 13.0%; Score 72; DB 2; Length 755;  
Best Local Similarity 27.5%; Pred. No. 36;  
Matches 25; Conservative 16; Mismatches 34; Indels 16; Gaps 4;  
A:Map position: 141

Qy 7 BOETKVR-----PKPLKLLKSVGAQKDTYTWKEVLHYLGQVIMTKRLVD-EKQOHIV 59  
Db 328 EYFSKVRQLDPEPKKRVLSVLQAGFD-BDRDFKYLHLSLEQSLKKAQMVAEADDSDHLD 386

A45604  
major blood-stage surface antigen Pv200 - Plasmodium vivax  
C:Species: Plasmodium vivax  
C>Date: 22-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C:Accession: A45604  
R:Gibson, H.L.; Tucker, J.E.; Kaelow, D.C.; Krettli, A.U.; Collins, W.E.; Kiefer, M.C.;  
Mol. Biochem. Parasitol. 50, 325-333, 1992  
A>Title: Structure and expression of the gene for Pv200, a major blood-stage surface antigen  
A:Reference number: A45604; MUID:92158013; PMID:1371329  
A:Accession: A45604  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1751 <GIB>  
A:CROSS-references: UNIPROT:Q26194; GB:M75674; NID:gl60608; PID:q457336  
A>Note: sequence extracted from NCBI backbone (NCBI:83591, NCBIP:83592)  
C:Superfamily: major merozoite surface antigen  
C:Keywords: surface antigen

Query Match 13.2%; Score 73; DB 2; Length 1751;  
Best Local Similarity 27.6%; Pred. No. 74;  
Matches 35; Conservative 20; Mismatches 42; Indels 30; Gaps 7;  
A:Map position: 141

Qy 4 PASEQETKVRPKP-----KLLKLLKSVGA-OKDTY----TWKEVLHYLGQVIMTKR 49  
Db 816 PPSPTAAVAAPAPTMSKLEYLEKLDPLKSAVACHKHIFVNTNMKKEL--LDQY----K 869

Qy 50 LYDEKQOHVRCNSNDKGLDGLFGVKS-----FSV-----KEHRKIYTYMYRNVLVVNQES 99  
Db 870 LNADQNKINETKCDLDELFFNVQNNLPAMYSIYDSMSNELQNLIELYQKEMVYNYKN 929

Qy 100 SDSGTSV 106  
Db 930 KDTDKKI 936

RESULT 7  
S58718  
probable nuclear protein YNL059c - yeast (Saccharomyces cerevisiae)  
N:Alternate names: protein N2430; protein YNL1620  
C:Species: Saccharomyces cerevisiae  
C>Date: 16-Feb-1996 #sequence\_revision 23-Feb-1996 #text\_change 09-Jul-2004  
C:Accession: S58718; S62987  
R:Bergez, P.; Doignon, F.; Crouzet, M.  
Yeast 11, 967-974, 1995  
A>Title: The sequence of a 44 420 bp fragment located on the left arm of chromosome XIV  
A:Reference number: S58711; MUID:96021608; PMID:8533472  
A:Accession: S58718  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-755 <BER>  
A:CROSS-references: UNIPROT:P53946; EMBL:U12141; NID:gl314216; PIDN:AAA99652.1; PID:g994  
A>Note: The nucleotide sequence was submitted to the EMBL Data Library, July 1994  
R:Bergez, P.; Doignon, F.; Crouzet, M.  
submitted to the Protein Sequence Database, April 1996  
A:Reference number: S62975  
A:Accession: S62987  
A:Molecule type: DNA  
A:Residues: 1-755 <BEW>  
A:CROSS-references: EMBL:L271335; NID:gl3101931; PID:e239897; PID:gl3101932; MIPS:YNL059c  
A:Experimental source: strain S288C  
C:Genetics:  
A:Gene: SGD:ARP5  
A:CROSS-references: SGD:S0005004; MIPS:YNL059c  
A:Map position: 141

Query Match 13.0%; Score 72; DB 2; Length 755;  
Best Local Similarity 27.5%; Pred. No. 36;  
Matches 25; Conservative 16; Mismatches 34; Indels 16; Gaps 4;  
A:Map position: 141

Qy 7 BOETKVR-----PKPLKLLKSVGAQKDTYTWKEVLHYLGQVIMTKRLVD-EKQOHIV 59  
Db 328 EYFSKVRQLDPEPKKRVLSVLQAGFD-BDRDFKYLHLSLEQSLKKAQMVAEADDSDHLD 386

Qy 60 KCSNDKGLDGLFGVKSFS-----VKHRK 82  
Db 387 EWNEDKTAQKFDLLDIAEDLNEDQIKERK 417

RESULT 8  
D71608  
hypochemical protein PFB0690w - malaria parasite (Plasmodium falciparum)  
C:Species: Plasmodium falciparum  
C>Date: 13-Nov-1998 #sequence\_revision 13-Nov-1998 #text\_change 09-Jul-2004  
C:Accession: D71608  
R:Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;  
Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.;  
Science 282, 1126-1132, 1998  
A>Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.  
A:Reference number: A71600; MUID:99021743; PMID:9804551  
A:Accession: D71608  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-244 <GAR>  
A:CROSS-references: UNIPROT:O96231; GB:AE001412; GB:AE001362; NID:g3845251; PIDN:AAC7192  
A:Experimental source: clone 3D7  
C:Genetics:  
A:Gene: PFB0690w

Query Match 12.9%; Score 71.5; DB 2; Length 244;  
Best Local Similarity 23.8%; Pred. No. 11;  
Matches 25; Conservative 24; Mismatches 47; Indels 9; Gaps 3;  
A:Map position: 1

Qy 6 SEQETKVRPKLKLKSVGAQKDTY-----TWKEVLHYLGQVIMTKRLVD-EKQOHIV- 59  
Db 94 SDYFKETETKSLKSLKMDNMKHKHFEHDTLEELVHMKHMQELETQYIKNDIENIFN 153

Qy 60 KCSNDK---LGDLFQVKSFSVKHRKIYTYMYRNVLVVNQESSD 101  
Db 154 ECINKDEYLKDTQERISVFKRKRQNKQCKLLIMKQNNKN 198

RESULT 9  
H96635  
unknown protein. 73054-77165 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: H96635  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Dewar, K.;  
anssen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Xu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: H96635  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-840 <STO>  
A:CROSS-references: UNIPROT:Q9C951; GB:AE005173; NID:g6751691; PIDN:AAF27674.1; GSPDB:GN  
C:Genetics:  
A:Gene: T7P1.16  
A:Map position: 1

Query Match 12.9%; Score 71.5; DB 2; Length 840;  
Best Local Similarity 19.3%; Pred. No. 45;  
Matches 21; Conservative 27; Mismatches 50; Indels 11; Gaps 2;  
A:Map position: 1

Qy 4 PASQETKVRPK---PKLLKLLKSVGAQKDTYTWKEVLHYLGQVIMTKRLVD-EKQOHIVK 60  
Db 192 PVVSASTKVRPNIGSKRLSLIKDVAARDASWHD-----LSSCDIIDRAQEILVN 243

Qy 61 CSNDKGLDGLFGVKSFSVKHRKIYTYMYRNVLVVNQESSDGSSTSVSEN 109



128 LENGTSALKN 137



RESULT 14  
ZHBPG4  
gene H protein - phage G4  
C;Species: Phage G4  
C;Date: 30-Nov-1979 #sequence\_revision 30-Nov-1979 #text\_change 09-Jul-2004  
C;Accession: A04255  
R;Godson, G.N.; Barrell, B.G.; Staden, R.; Fiddes, J.C.  
Nature 276, 236-247, 1978  
A;Title: Nucleotide sequence of bacteriophage G4 DNA.  
A;Reference number: A93200; MUID:79053264; PMID:714153  
A;Accession: A04255  
A;Molecule type: DNA  
A;Residues: 1-337 <GOD>  
A;Cross-references: UNIPROT:P03647; GB:J02454; GB:M10724; GB:M11404; GB:V00657; NID:g158  
C;Comment: Gene H protein is the minor spike component of the viral shell.  
C;Superfamily: phage phi-X174 gene H protein

Query Match 12.6%; Score 70; DB 1; Length 337;  
Best Local Similarity 21.8%; Pred. NO. 22;  
Matches 26; Conservative 19; Mismatches 44; Indels 30; Gaps 3;

QY 20 KLLKSVGKQKDYTM-KEVLHYL-----GQYIMTKEL 50  
||::||| | : || | : ||  
Db 94 KLMEAVGLSKASDKGDKDYLAAPFELNPFWRERAGAGASSPGMQDAGFQNKELTRMQ 153  
||::||| | : || | : ||

QY 51 YDEKQOHIVKCSNDKLGDFGVKSPVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 109  
||::||| | : || | : ||  
Db 154 LD-NQKETAKQNETQKEIAGLQISITSRENTKYDYAQNEMLAYNQKESMSRVGAILEN 211  
||::||| | : || | : ||

RESULT 15  
S70186  
21K protein - Shigella flexneri  
C;Species: Shigella flexneri  
C;Date: 12-Feb-1998 #sequence\_revision 20-Feb-1998 #text\_change 09-Jul-2004  
C;Accession: S70186  
R;Uchiya, K.; Tobe, T.; Komatsu, K.; Suzuki, T.; Watarai, M.; Fukuda, I.; Yoshikawa, M.;  
Mol. Microbiol. 17, 241-250, 1995  
A;Title: Identification of a novel virulence gene, virA, on the large plasmid of Shigella  
A;Reference number: S70186; MUID:96079274; PMID:7494473  
A;Accession: S70186  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-187 <UCH>  
A;Cross-references: UNIPROT:Q52296; EMBL:D26468; NID:g992954; PIDN:BAA05481.1; PID:d1006  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1994

Query Match 12.5%; Score 69; DB 2; Length 187;  
Best Local Similarity 21.6%; Pred. No. 14;  
Matches 21; Conservative 17; Mismatches 31; Indels 28; Gaps 3;

QY 23 KSVGAKQDYTMKEVLHYLGVYIMTKRLYDEKQ-----HIVKCSNDKL 66  
: ||::||| | : || | : ||  
Db 40 RSARAQRDDWLKKEIL-----RVYDNHQVYAVRVKVMHQLREGIRVACTVARL 89  
: ||::||| | : || | : ||

QY 67 GDLFGVKSFSVKEHRKIYTMIRNLVNVNQESSDSG 103  
: ||::||| | : || | : ||  
Db 90 MAVMGLA--GVLRGKKVHTVSRKAAAGDRVNRHQG 124  
: ||::||| | : || | : ||

Search completed: January 27, 2005, 18:15:12  
Job time : 20.8 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 27, 2005, 17:51:46 ; Search time 84.6 Seconds  
(without alignments)  
741.322 Million cell updates/sec

Title: US-10-822-254-12  
Perfect score: 554  
Sequence: 1 SQIPASEQETKVRPKLLK.....NLVVNQESSDSGTSVSEN 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 02:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	511	92.2	166	Q8NDW2	Q8ndw2 homo sapien
2	511	92.2	195	Q96DS4	Q96ds4 homo sapien
3	511	92.2	243	Q8TE47	Q8te47 homo sapien
4	511	92.2	491	1 MDM2_HUMAN	Q00987 homo sapien
5	511	92.2	491	2 AAP35922	Aap35922 homo sapi
6	511	92.2	491	2 AAH67077	Aah67077 homo sapi
7	499	90.1	487	1 MDM2_CANFA	P56950 canis famil
8	499	90.1	487	2 Q9GMZ6	Q9gmz6 canis famil
9	499	90.1	491	1 MDM2_HORSE	P56951 equus cabal
10	496	89.5	491	2 Q7YRZ8	Q7yrz8 felis silve
11	461	83.2	436	2 Q8WYJ2	Q8wyj2 homo sapien
12	451.5	81.5	489	1 MDM2_MOUSE	P23804 mus musculu
13	451.5	81.5	489	2 Q91XK7	Q91xk7 m mus muscu
14	434	78.3	118	2 Q8WYJ3	Q8wyj3 homo sapien
15	433.5	78.2	466	1 MDM2_MESAU	Q60524 mesocricetu
16	387	69.9	325	2 Q9PVL2	Q9pvl2 gallus gall
17	365	65.9	173	2 Q8TE46	Q8te46 homo sapien
18	346	62.5	473	1 MDM2_XENLA	P56273 xenopus lae
19	346	62.5	473	2 Q6GMB5	Q6gmb5 xenopus lae
20	345	62.3	482	2 Q6P3Q9	Q6p3q9 xenopus tro
21	345	62.3	482	2 AAH63898	Aah63898 xenopus t
22	311	56.1	105	2 Q8NDW0	Q8ndw0 homo sapien
23	297	53.6	426	2 Q9CK41	Q9ck41 canis famil
24	287.5	51.9	445	1 MDM2_BRARE	O42354 brachydanio
25	287.5	51.9	445	2 AAAM00198	Aam00198 brachydanio
26	281	50.7	491	2 Q7ZUW7	Q7zuw7 brachydanio
27	278.5	50.3	489	1 MDM4_MOUSE	Q35618 mus musculu
28	275.5	49.7	489	2 Q9CYG1	Q9cyg1 m mus muscu
29	270	48.7	475	2 Q7Z1I3	Q7z1i3 xenopus lae
30	269	48.6	490	2 Q99L86	Q99l86 mus musculu
31	268.5	48.5	446	2 Q8WYJ1	Q8wyj1 homo sapien

#### RESULT 1

Q8NDW2 ID Q8NDW2 PRELIMINARY; PRT; 166 AA.  
AC Q8NDW2;  
DT 01-OCT-2002 (Tremblrel. 22, Created)  
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)  
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
DE P53-binding protein.  
GN Name=MDM2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bartel F., Pinkert D., Kappeler M., Bache M., Schmidt H., Taubert H.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ491698; CAD36959.1; -.  
DR HSP; Q9UMT8; 1YCR.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR InterPro; IPR0010984; MDM2.  
DR InterPro; IPR003121; SWIB\_MDM2.  
DR Pfam; PF02201; SWIB; 1  
SQ SEQUENCE 166 AA; 18900 MW; FA6B5BA18E85040D CRC64;

Query Match 92.2%; Score 511; DB 2; Length 166;  
Best Local Similarity 94.5%; Pred. No. 4.6e-43;  
Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 SQIPASEQETKVRPKLLKLLKSVGAOKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIVK 60  
Db 17 SQIPASEQETLVRPKLLKLLKSVGAOKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIVY 76  
QY 61 CSNDKLGDLGVKSFVSKHEHRIYMIYRNLVVNVNQESSDSGTSVSEN 109  
Db 77 CSNDLLGDLGVKSFVSKHEHRIYMIYRNLVVNVNQESSDSGTSVSEN 125

#### RESULT 2

Q96DS4 ID Q96DS4 PRELIMINARY; PRT; 195 AA.  
AC Q96DS4;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
DE MDM2 variant FB26.  
GN Name=MDM2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Rhabdomyosarcoma tumor;

RA Bartel F., Taylor A.C., Taubert H., Harris L.C.;  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF385323; AAL3243.1; -;  
 DR HSSP; Q9UMT8; 1YCR.

DR GO; GO:0005634; C:nucleus; IEA.

DR InterPro; IPR010984; MDM2.

DR InterPro; IPR003121; SWTB\_MDM2.

DR Pfam; PF02201; SWTB; 1.

SQ SEQUENCE 195 AA; 22161 MW; 4987AE567DB12D5D CRC64;

Query Match 92.2%; Score 511; DB 2; Length 195;

Best Local Similarity 94.5%; Pred. No. 5.5e-43;

Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIYK 60

Db 17 SQIPASEQETLVRPRLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIY 76

OY 61 CSNDKLGDLFGVKSFSVKEHKRIYTMIRNLVNVNQSSDSGTSVSEN 109

Db 77 CSNDLLGDLFGVPSFSVKEHKRIYTMIRNLVNVNQSSDSGTSVSEN 125

# RESULT 3

QBTE47

ID QBTE47 PRELIMINARY; PRT; 243 AA.

AC QBTE47; PRELIMINARY; PRT; 243 AA.

DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE MDM2 isoform KB9 protein.

GN Name=MDM2 isoform KB9;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN (1)

RP SEQUENCE FROM N.A.

RC TISSUE=Lymphocytes;

RA Bartel F., Pinkert D., Kappler M., Bache M., Schmidt H., Taubert H.;

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ3430612; CAD23251.1; -;

DR HSSP; Q9UMT8; 1YCR.

DR GO; GO:0005634; C:nucleus; IEA.

DR GO; GO:000151; C:ubiquitin ligase complex; IEA.

DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.

DR GO; GO:0008270; F:zinc ion binding; IEA.

DR GO; GO:0016567; P:protein ubiquitination; IEA.

DR InterPro; IPR010984; MDM2.

DR InterPro; IPR003121; SWTB\_MDM2.

DR Pfam; PF02201; SWTB; 1.

DR SMART; SM00184; RING; 1.

DR PROSITE; PS50089; ZF\_RING\_2; 1.

SQ SEQUENCE 243 AA; 27317 MW; 9EB5D0142CF185A2 CRC64;

Query Match

Best Local Similarity 92.2%; Score 511; DB 2; Length 243;

Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIYK 60

Db 17 SQIPASEQETLVRPRLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIY 76

OY 61 CSNDKLGDLFGVKSFSVKEHKRIYTMIRNLVNVNQSSDSGTSVSEN 109

Db 77 CSNDLLGDLFGVPSFSVKEHKRIYTMIRNLVNVNQSSDSGTSVSEN 125

# RESULT 4

MDM2\_HUMAN

ID MDM2\_HUMAN STANDARD; PRT; 491 AA.

AC Q00987; Q13226; Q13297; Q13298; Q13299; Q13300; Q13301; Q9UG13;

AC Q9UMT8;

DT 01-APR-1993 (Rel. 25, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 01-OCT-2004 (Rel. 45, Last annotation update)

DE Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein

Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Hdm2).

GN Name=MDM2;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN (1)

RP SEQUENCE FROM N.A. (ISOFORM MDM2).

RE MEDLINE=92310576; PubMed=1614537;

RA Oliner J.D., Kinzler K.W., Meltzer P.S., George D.L., Vogelstein B.;

RT "Amplification of a gene encoding a p53-associated protein in human

sarcomas.";

RL Nature 358:80-83 (1992).

RN (2)

RP SEQUENCE FROM N.A. (ISOFORMS MDM2-A; -B; -C; -D AND -E).

RC TISSUE=Ovarian carcinoma;

RE MEDLINE=96313107; PubMed=8705862;

RA Sigalas I., Calvert A.H., Anderson J.J., Neal D.E., Lunec J.;

RT "Alternatively spliced mdm2 transcripts with loss of p53 binding

domain sequences: transforming ability and frequent detection in human

cancer.";

RL Nat. Med. 2:912-917 (1996).

RN (3)

RP SEQUENCE FROM N.A. (ISOFORM MDM2-ALPHA).

RE MEDLINE=20065171; PubMed=10597303;

RA Veidhoen N., Metcalfe S., Milner J.;

RT "A novel exon within the mdm2 gene modulates translation initiation in

vitro and disrupts the p53-binding domain of mdm2 protein.";

RL Oncogene 18:7026-7033 (1999).

RN (4)

RP SEQUENCE FROM N.A. (ISOFORM MDM2).

RE MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN (6)

RP SEQUENCE OF 6-491 FROM N.A. (ISOFORM MDM2-A1).

RA Liang H., Atkins H., Abdel-Fattah R., Saueyun R., Lunec J.;

RT "Genomic organisation of the human MDM2 oncogene and relationship to

its alternatively spliced mRNA's.";

RT Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

RN (7)

RP SEQUENCE OF 1-24 FROM N.A.  
 RX MEDLINE=95380270; PubMed=7551818;  
 RA Zauberman A., Flusberg D., Haupt Y., Barak Y., Oren M.;  
 RT "A functional p53-responsive intronic promoter is contained within the  
 human mdm2 gene.";  
 RL Nucleic Acids Res. 23:2584-2592(1995).  
 RN [8]  
 RP SEQUENCE OF 1-9 FROM N.A.  
 RX MEDLINE=97413643; PubMed=9270029;  
 RA Landers J.E., Cassel S.L., George D.L.;  
 RT "Translational enhancement of mdm2 oncogene expression in human tumor  
 cells containing a stabilized wild-type p53 protein.";  
 RL Cancer Res. 57:3562-3568(1997).  
 RN [9]  
 RP SEQUENCE OF 301-481 FROM N.A.  
 RX MEDLINE=20542019; PubMed=11087894;  
 RA Taubert H., Kappler M., Meyer A., Bartel F., Schlott T.,  
 RA Lautenschlaeger C., Bache M., Schmidt H., Wuerl P.;  
 RT "A MboII polymorphism in exon 11 of the human MDM2 gene occurring in  
 normal blood donors and in soft tissue sarcoma patients: an indication  
 for an increased cancer susceptibility?";  
 RL Mutat. Res. 456:39-44(2000).  
 RN [10]  
 RP MUTAGENESIS OF CYS-464.  
 RX MEDLINE=98111004; PubMed=9450543;  
 RA Honda R., Tanaka H., Yasuda H.;  
 RT "Oncoprotein MDM2 is a ubiquitin ligase E3 for tumor suppressor p53.";  
 RL FEBS Lett. 420:25-27(1997).  
 RN [11]  
 RP MUTAGENESIS OF CYS-449.  
 RX MEDLINE=20190101; PubMed=10723139;  
 RA Honda R., Yasuda H.;  
 RT "Activity of MDM2, a ubiquitin ligase, toward p53 or itself is  
 dependent on the RING finger domain of the ligase.";  
 RL Oncogene 19:1473-1476(2000).  
 RN [12]  
 RP MUTAGENESIS.  
 RX MEDLINE=20187618; PubMed=1072742;  
 RA Fang S., Jensen J.P., Ludwig R.L., Vousden K.H., Weissman A.M.;  
 RT "Mdm2 is a RING finger-dependent ubiquitin protein ligase for itself  
 and p53.";  
 RL J. Biol. Chem. 275:8945-8951(2000).  
 RN [13]  
 RP MUTAGENESIS OF CYS-441 AND CYS-478.  
 RX MEDLINE=20076498; PubMed=10608892;  
 RA Sharp D.A., Kratowicz S.A., Sank M.J., George D.L.;  
 RT "Stabilization of the MDM2 oncoprotein by interaction with the  
 structurally related MDMX protein.";  
 RL J. Biol. Chem. 274:38189-38196(1999).  
 RN [14]  
 RP NUCLEOLAR LOCALIZATION SIGNAL.  
 RX MEDLINE=20173879; PubMed=10707090;  
 RA Lohrum M.A.E., Ashcroft M., Kubbutat M.H.G., Vousden K.H.;  
 RT "Identification of a cryptic nucleolar-localization signal in MDM2.";  
 RL Nat. Cell Biol. 2:179-181(2000).  
 RN [15]  
 RP PHOSPHORYLATION BY ATM.  
 RX MEDLINE=20079591; PubMed=10611322;  
 RA Khosravi R., Maya R., Gottlieb T., Oren M., Shiloh Y., Shkedy D.;  
 RT "Rapid ATM-dependent phosphorylation of MDM2 precedes p53 accumulation  
 in response to DNA damage.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 96:14973-14977(1999).  
 RN [16]  
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 25-109 IN COMPLEX WITH P53.  
 RX MEDLINE=97081050; PubMed=8875929;  
 RA Kusie P.H., Gorina S., Marechal V., Elenbaas B., Moreau J.,  
 RA Levine A.J., Pavletich N.P.;  
 RT "Structure of the MDM2 oncoprotein bound to the p53 tumor suppressor  
 transactivation domain.";  
 RL Science 274:948-953(1996).  
 CC -1- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and  
 apoptosis by binding its transcriptional activation domain.  
 CC Functions as a ubiquitin ligase E3, in the presence of E1 and E2,

CC toward p53 and itself. Permits the nuclear export of p53 and  
 CC targets it for proteasome-mediated proteolysis.  
 CC -1- COFACTOR: Zinc is required for ubiquitin ligase E3 activity.  
 CC -1- SUBUNIT: Binds p53, p73, ARF(p14), ribosomal protein L5 and  
 CC specifically to RNA. Can interact also with retinoblastoma protein  
 CC (RB), E1A-associated protein EP300 and the E2F1 transcription  
 CC factor.  
 CC -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed  
 CC predominantly in the nucleoplasm. Interaction with ARF(p14)  
 CC results in the localization of both proteins to the nucleolus. The  
 CC nucleolar localization signals in both ARF(p14) and MDM2 may be  
 CC necessary to allow efficient nucleolar localization of both  
 CC proteins.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=8;  
 CC Name=Mdm2;  
 CC IsoId=Q00987-1; Sequence=Displayed;  
 CC Name=Mdm2-A;  
 CC IsoId=Q00987-2; Sequence=VSP\_003208;  
 CC Name=Mdm2-A1;  
 CC IsoId=Q00987-3; Sequence=VSP\_003208, VSP\_003214;  
 CC Name=Mdm2-B;  
 CC IsoId=Q00987-4; Sequence=VSP\_003209;  
 CC Name=Mdm2-C;  
 CC IsoId=Q00987-5; Sequence=VSP\_003211;  
 CC Name=Mdm2-D;  
 CC IsoId=Q00987-6; Sequence=VSP\_003210;  
 CC Name=Mdm2-E;  
 CC IsoId=Q00987-7; Sequence=VSP\_003212, VSP\_003213;  
 CC Name=Mdm2-alpha;  
 CC IsoId=Q00987-8; Sequence=VSP\_003207;  
 CC -1- TISSUE SPECIFICITY: Ubiquitous. Isoforms MDM2-A, -B, -C, -D and -E  
 CC are observed in a range of human cancers but absent in normal  
 CC tissues.  
 CC -1- INDUCTION: By DNA damage.  
 CC -1- DOMAIN: Region I is sufficient for binding p53 and inhibiting its  
 CC G1 arrest and apoptosis functions. It also binds p73 and E2F1.  
 CC Region II contains most of a central acidic region required for  
 CC interaction with ribosomal protein L5 and a putative C4-type zinc  
 CC finger. The RING finger domain which coordinates two molecules of  
 CC zinc interacts specifically with RNA whether or not zinc is  
 CC present and mediates the hetero-oligomerization with MDM4. It is  
 CC also essential for its ubiquitin ligase E3 activity toward p53 and  
 CC itself.  
 CC -1- PTM: Phosphorylated in response to ionizing radiation in an ATM-  
 CC dependent manner.  
 CC -1- DISEASE: Seems to be amplified in certain tumors (including soft  
 CC tissue sarcomas, osteosarcomas and gliomas). A higher frequency of  
 CC splice variants lacking p53 binding domain sequences was found in  
 CC late-stage and high-grade ovarian and bladder carcinomas. Four of  
 CC the splice variants show loss of p53 binding.  
 CC -1- MISCELLANEOUS: MDM2 RING finger mutations that failed to  
 CC Query Match 92.2%; Score 511; DB 1; Length 491;  
 CC Best Local Similarity 94.5%; Pred. No. 1.5e-42;  
 CC Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 Qy 1 SQIPASEQETKVRPKPLKLLKSVGAQKQYTMKEVLHLYGQYTMTRLYDEKQOHVVK 60  
 Db 17 SQIPASQETLVVRPKPLLLKLLKSVGAQKQYTMKEVLHLYGQYTMTRLYDEKQOHVY 76  
 Qy 61 CSNDKLGDLFGVKSFSVKEHRKIYTMIRNLVVVNQQSSDSGTSVSEN 109  
 Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVVNQQSSDSGTSVSEN 125  
 RESULT 5  
 AAP35922  
 ID AAP35922 PRELIMINARY; PRT; 491 AA.  
 AC AAP35922;  
 DT 02-MAR-2004 (TRENBLrel. 27, Created)  
 DT 02-MAR-2004 (TRENBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TRENBLrel. 27, Last annotation update)

Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (Mouse).

DE Homo sapiens (Human).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. CC NCBI\_TaxID=9606; CC [1]

RP SEQUENCE FROM N.A.

RA Kainine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S., RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y., RA Phelan M., Farmer A.;

RT "Cloning of human full-length CDSs in BD Creator(TM) System Donor vector.;"

RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BT007258; AAP35922.1; -. CC

SQ SEQUENCE 491 AA; 55232 MW; F37CE163876BC983 CRC64;

Query Match 92.2%; Score 511; DB 2; Length 491;

Best Local Similarity 94.5%; Pred. No. 1.5e-42;

Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 SQIPASEQETKVRPKPLKLLKLSVGAQKDTYTMKEVLYHLYGVYIMTKRLYDEKQHIYK 60

DB 17 SQIPASEQETLVRPKPLKLLKLSVGAQKDTYTMKEVLYHLYGVYIMTKRLYDEKQHIYV 76

QY 61 CSNDKLGDLFGVKSFSVKEHRKIYTMIRNLVVVNQOESSDGSVSSEN 109

DB 77 CSNDLLGDLFGVKSFSVKEHRKIYTMIRNLVVVNQOESSDGSVSSEN 125

RESULT 6

AAH67077 PRELIMINARY; PRT; 491 AA.

AC AAH67077; DT 14-APR-2004 (TrEMBLrel. 27, Created)

DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)

DT 14-APR-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. CC NCBI\_TaxID=9606; CC [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Muscle; CC

RX MEDLINE=22388257; PubMed=12477932; CC

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., CC

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., CC

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., CC

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P., CC

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., CC

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., CC

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., CC

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., CC

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., CC

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., CC

RA Villalón D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A., CC

RA Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A., CC

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., CC

RA Blakesley R.C., Touchman J.W., Green E.D., Dickson M.C., CC

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., CC

RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E., CC

RA Jones S.J., Marra M.A.; CC

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.;"

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). CC

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Muscle; CC

RA Strausberg R.; CC

RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases. CC

DR EMBL; BC067077; AAH67077.1; -. CC

KW Hypothetical protein.

Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (Mouse).

DE Homo sapiens (Human).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. CC NCBI\_TaxID=9606; CC [1]

RP SEQUENCE FROM N.A.

RA Kainine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S., RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y., RA Phelan M., Farmer A.;

RT "Cloning of human full-length CDSs in BD Creator(TM) System Donor vector.;"

RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BT007258; AAP35922.1; -. CC

SQ SEQUENCE 491 AA; 55232 MW; F37CE163876BC983 CRC64;

Query Match 92.2%; Score 511; DB 2; Length 491;

Best Local Similarity 94.5%; Pred. No. 1.5e-42;

Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 SQIPASEQETKVRPKPLKLLKLSVGAQKDTYTMKEVLYHLYGVYIMTKRLYDEKQHIYK 60

DB 17 SQIPASEQETLVRPKPLKLLKLSVGAQKDTYTMKEVLYHLYGVYIMTKRLYDEKQHIYV 76

QY 61 CSNDKLGDLFGVKSFSVKEHRKIYTMIRNLVVVNQOESSDGSVSSEN 109

DB 77 CSNDLLGDLFGVKSFSVKEHRKIYTMIRNLVVVNQOESSDGSVSSEN 125

RESULT 7

MDM2\_CANFA STANDARD; PRT; 487 AA.

AC P56950; Q95KN5; DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Cdm2). CC

GN Name=Mdm2; CC

OS Canis familiaris (Dog). CC

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis. CC NCBI\_TaxID=9615; CC [1]

RP SEQUENCE OF 1-484 FROM N.A.

RX MEDLINE=20218866; PubMed=10754200; CC

RA Nasir L., Burr P.D., McFarlane S.T., Gault E., Thompson H., CC

RA Argyle D.J.; CC

RT "Cloning, sequence analysis and expression of the cDNAs encoding the canine and equine homologues of the mouse double minute 2 (mdm2) proto-oncogene.;"

RT proto-oncogene.;"

RL Cancer Lett. 152:9-13(2000). CC

RN [2]

RP SEQUENCE FROM N.A. (ISOFORMS MDM2 AND MDM2-ALPHA). CC

RX MEDLINE=20065171; PubMed=10597303; CC

RA Veldhoen N., Metcalfe S., Milner J.; CC

RT "A novel exon within the mdm2 gene modulates translation initiation in vitro and disrupts the p53-binding domain of mdm2 protein.;"

RL Oncogene 18:7026-7033(1999). CC

CC -1- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and apoptosis by binding its transcriptional activation domain. CC

CC Functions as a ubiquitin ligase E3, in the presence of E1 and E2, toward p53 and itself. Permits the nuclear export of p53 and targets it for proteasome-mediated proteolysis (By similarity). CC

CC -1- COFACTOR: Zinc is required for ubiquitin ligase E3 activity (By similarity). CC

CC -1- SUBUNIT: Binds p53, p73, ARF(P14), ribosomal protein L5 and specifically to RNA. Can interact also with retinoblastoma protein (RB), E1A-associated protein EP300 and the E2F1 transcription factor (By similarity). CC

CC -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed predominantly in the nucleoplasm (By similarity). CC

CC -1- ALTERNATIVE PRODUCTS: CC

CC Event-Alternative splicing; Named isoforms=2; CC

CC Name=Mdm2; CC

CC IsoId=P56950-1; Sequence=Displayed; CC

CC Name=Mdm2-alpha; CC

CC IsoId=P56950-2; Sequence=VSP 003206; CC

CC -1- TISSUE SPECIFICITY: Isoform Mdm2-alpha is present in lymphoid and CC

CC testicular tissues. CC

CC -1- DOMAIN: Region I is sufficient for binding p53 and inhibiting its CC

CC G1 arrest and apoptosis functions. It also binds p73 and E2F1. CC

CC Region II contains most of a central acidic region required for CC

CC interaction with ribosomal protein L5 and a putative C4-type zinc CC

CC finger. The RING finger domain which coordinates two molecules of CC

CC zinc interacts specifically with RNA whether or not zinc is CC

CC present and mediates the hetero-oligomerization with MDM4. It is CC

also essential for its ubiquitin ligase E3 activity toward p53 and itself (By similarity).

-!- SIMILARITY: Belongs to the MDM2 / MDM4 family.

-!- SIMILARITY: Contains 1 RanBP2-type zinc finger.

-!- SIMILARITY: Contains 1 RING-type zinc finger.

-!- SIMILARITY: Contains 1 SWIB domain.

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EMBL; AF100705; AAF67833.1; -.

EMBL; AF322416; AAG42840.1; -.

HSSP; Q9UMT8; LYCR.

InterPro; IPR010984; MDM2.

InterPro; IPR003121; SWIB.

InterPro; IPR001876; Znf\_RanGDP.

InterPro; IPR001841; Znf\_ring.

Pfam; PF02201; SWIB; 1.

Pfam; PF00641; zf-RanBP; 1.

SMART; SM00184; RING; 1.

PROSITE; PS01358; ZF\_RANBP2\_1; 1.

PROSITE; PS0199; ZF\_RANBP2\_2; 1.

PROSITE; PS00518; ZF\_RING\_1; FALSE\_NEG.

PROSITE; PS00089; ZF\_RING\_2; 1.

KW Alternative splicing; Ligase; Metal-binding; Nuclear protein;

KW Ub1 conjugation pathway; Zinc; Zinc-finger.

FT DOMAIN 27 107

FT DOMAIN 179 185 Nuclear localization signal (Potential).

FT DOMAIN 190 202 Nuclear export signal.

FT DOMAIN 210 304 ABF-binding.

FT DOMAIN 210 215 Poly-Ser.

FT DOMAIN 242 331 Region II.

FT DOMAIN 243 301 Asp/Glu-rich (acidic).

FT ZN\_FING 299 328 RanBP2-type.

FT ZN\_FING 434 475 RING-type.

FT DOMAIN 462 469 Nucleolar localization signal (Potential).

FT VARSPLIC 1 61 Missing (in isoform Mdm2-alpha).

FT CONFLICT 11 11 /FTID=VSP\_003206.

FT CONFLICT 238 239 G -> D (in Ref. 2).

SQ SEQUENCE 487 AA; 54696 MW; 60CDB470A32A8E69 CRC64;

Query Match 90.1%; Score 499; DB 1; Length 487;

Best Local Similarity 91.7%; Pred. No. 2.4e-41;

Matches 100; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHVYK 60

DB 17 SQIPASEQETLVRPKPKLLKLLKSVGAQKDTYTMKEVIFYLQYIMTKRLYDEKQOHVY 76

QY 61 CSNDKLGDLFGVKFSVKEHRIYMIYRNLVVNVNQSSDSTSVSEN 109

DB 77 CSNDLLGDLFGVPSFVKEHRIYMIYRNLVVNVNQHPSPDSTSVSEN 125

RESULT 8

Q9GMZ6 PRELIMINARY; PRT; 487 AA.

AC Q9GMZ6

DT 01-MAR-2001 (TRENBLrel. 16, Created)

DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)

DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)

DE MDM2.

GN Name=mdm2;

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI\_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RA Setouchi A., Tsujimoto H.;

RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB031276; BAB11975.1; -.

DR HSSP; Q9UMT8; LYCR.

DR GO; GO:0005730; C:nucleolus; ISS.

DR GO; GO:0005654; C:nucleoplasm; ISS.

DR GO; GO:0017163; F:negative regulator of basal transcription a. . .; ISS.

DR GO; GO:0005515; F:protein binding; ISS.

DR GO; GO:0000122; F:negative regulation of transcription from P. . .; ISS.

DR InterPro; IPR010984; MDM2.

DR InterPro; IPR003121; SWIB\_MDM2.

DR InterPro; IPR001876; Znf\_RanGDP.

DR Pfam; PF02201; SWIB; 1.

DR Pfam; PF00641; zf-RanBP; 1.

DR SMART; SM00184; RING; 1.

DR PROSITE; PS01358; ZF\_RANBP2\_1; 1.

DR PROSITE; PS0199; ZF\_RANBP2\_2; 1.

DR PROSITE; PS00089; ZF\_RING\_2; 1.

SQ SEQUENCE 487 AA; 54724 MW; 34FC5CC6A18D7744 CRC64;

Query Match 90.1%; Score 499; DB 2; Length 487;

Best Local Similarity 91.7%; Pred. No. 2.4e-41;

Matches 100; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHVYK 60

DB 17 SQIPASEQETLVRPKPKLLKLLKSVGAQKDTYTMKEVIFYLQYIMTKRLYDEKQOHVY 76

QY 61 CSNDKLGDLFGVKFSVKEHRIYMIYRNLVVNVNQSSDSTSVSEN 109

DB 77 CSNDLLGDLFGVPSFVKEHRIYMIYRNLVVNVNQHPSPDSTSVSEN 125

RESULT 9

ID MDM2\_HORSE STANDARD; PRT; 491 AA.

AC P56951;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Edm2).

DE Name=MDM2;

OS Equus caballus (Horse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Perissodactyla; Equidae; Equus.

OX NCBI\_TaxID=9796;

RN [1]

RP SEQUENCE FROM N.A.

RA Nasir L., Burr P.D., McFarlane S.T., Gault E., Thompson H., Argyle D.J.;

RT "Cloning, sequence analysis and expression of the cDNAs encoding the canine and equine homologues of the mouse double minute 2 (mdm2) proto-oncogene."

RT Cancer Lett. 152:9-13(2000).

CC -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and apoptosis by binding its transcriptional activation domain.

CC Functions as a ubiquitin ligase E3, in the presence of E1 and E2, toward p53 and itself. Permits the nuclear export of p53 and targets it for proteasome-mediated proteolysis (By similarity).

CC -!- COPACATOR: Zinc is required for ubiquitin ligase E3 activity (By similarity).

CC -!- SUBUNIT: Binds p53, p73, ARF(p14), ribosomal protein L5 and specifically to RNA. Can interact also with retinoblastoma protein (RB), E1a-associated protein EP300 and the E2F1 transcription factor (By similarity).

CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed

predominantly in the nucleoplasm (By similarity).

-!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its G1 arrest and apoptosis functions. It also binds p73 and E2F1. Region II contains most of a central acidic region required for interaction with ribosomal protein L5 and a putative C4-type zinc finger. The RING finger domain which coordinates two molecules of zinc interacts specifically with RNA whether or not zinc is present and mediates the hetero-oligomerization with MDM4. It is also essential for its ubiquitin ligase E3 activity toward p53 and itself (By similarity).

-!- SIMILARITY: Belongs to the MDM2 / MDM4 family.

-!- SIMILARITY: Contains 1 RANBP2-type zinc finger.

-!- SIMILARITY: Contains 1 RING-type zinc finger.

-!- SIMILARITY: Contains 1 SWIB domain.

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-----

EMBL; AF121140; RANBP2866.1; -.

DR HSP; Q9UMT8; 1YCR.

DR InterPro; IPR010984; MDM2.

DR InterPro; IPR003121; SWIB.

DR InterPro; IPR001876; Znf\_RanGDP.

DR InterPro; IPR001841; Znf\_Ring.

DR Pfam; PF02201; SWIB; 1.

DR Pfam; PF00641; zf-RanBP; 1.

DR SMART; SM00184; RING; 1.

DR PROSITE; PS01358; ZF\_RANBP2\_1; 1.

DR PROSITE; PS01999; ZF\_RANBP2\_2; 1.

DR PROSITE; PS00518; ZF\_RING\_1; FALSE\_NEG.

DR PROSITE; PS50089; ZF\_RING\_2; 1.

DR Ligase; Metal-binding; Nuclear protein; Ubl conjugation pathway; Zinc; Zinc-finger.

KW DOMAIN 27 107 SWIB.

FT DOMAIN 179 185 Nuclear localization signal (Potential);

FT DOMAIN 190 202 Nuclear export signal.

FT DOMAIN 210 304 ARF-binding.

FT DOMAIN 210 215 Poly-Ser.

FT DOMAIN 242 331 Region II.

FT DOMAIN 243 301 Asp/Glu-rich (acidic).

FT ZN\_FING 299 328 RANBP2-type.

FT ZN\_FING 438 479 RING-type.

FT DOMAIN 466 473 Nucleolar localization signal (Potential).

FT SEQUENCE 491 AA; 55279 MW; 641B033D5C1DEC39 CRC64;

Query Match 90.1%; Score 499; DB 1; Length 491;

Best Local Similarity 91.7%; Pred. No. 2.4e-41;

Matches 100; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 SQIPASEQETKVRPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIVK 60

Db 17 SQIPASEQETLVRPKLLKLLKSVGAQKDTYTMKEVIFYLQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDKLGDLFGVKSFSVKEHRKIYTMIRNLVVVNQOESSDSGTSVSEN 109

Db 77 CSNDLLGDLFGVPSFVSKEHRKIYTMIRNLVVVNQOEPSDSGTSVSEN 125

RESULT 10

Q7YRZ8 PRELIMINARY; PRT; 491 AA.

AC Q7YRZ8; (T-EMBLrel. 25, Created)

DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)

DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)

DE Double minute 2 protein MDM2.

GN Name=mdm2;

OS Felis silvestris catus (Cat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.

OX NCBI\_TaxID=9685;

RN [1]

RP SEQUENCE FROM N.A.

RA Miki R., Okuda M., Ma Z., Inokuma H., Onishi T.;

RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB099709; BAC78209.1; -.

DR GO; GO:0005730; C:nucleolus; ISS.

DR GO; GO:0005654; C:nucleoplasm; ISS.

DR GO; GO:0017163; P:negative regulator of basal transcription a. . .; ISS.

DR GO; GO:0005515; F:protein binding; ISS.

DR GO; GO:0000122; P:negative regulation of transcription from P. . .; ISS.

DR InterPro; IPR003121; SWIB MDM2.

DR InterPro; IPR001876; Znf\_RanGDP.

DR InterPro; IPR001841; Znf\_Ring.

DR Pfam; PF02201; SWIB; 1.

DR Pfam; PF00641; zf-RanBP; 1.

DR SMART; SM00184; RING; 1.

DR PROSITE; PS01358; ZF\_RANBP2\_1; 1.

DR PROSITE; PS01999; ZF\_RANBP2\_2; 1.

DR PROSITE; PS50089; ZF\_RING\_2; 1.

SQ SEQUENCE 491 AA; 55433 MW; D93E25D638E88934 CRC64;

Query Match 89.5%; Score 496; DB 2; Length 491;

Best Local Similarity 90.8%; Pred. No. 4.9e-41;

Matches 99; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 SQIPASEQETKVRPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIVK 60

Db 17 SQIPASEQETLVRPKLLKLLKSVGAQKDTYTMKEVIFYLQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDKLGDLFGVKSFSVKEHRKIYTMIRNLVVVNQOESSDSGTSVSEN 109

Db 77 CSNDLLGDLFGVPSFVSKEHRKIYTMIRNLVVVNQOEPSDSGTSVSEN 125

RESULT 11

Q8WYJ2 PRELIMINARY; PRT; 436 AA.

AC Q8WYJ2; (T-EMBLrel. 20, Created)

DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)

DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)

DE MDM2 protein.

GN Name=MDM2;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21248713; PubMed=11351297;

RA Tamborini E., Della Torre G., Lavarino C., Azzarelli A.,

RA Carpinelli P., Pierotti M.A., Pilotti S.;

RT "Analysis of the molecular species generated by MDM2 gene amplification in liposarcomas.";

RL Int. J. Cancer 92:790-796(2001).

DR EMBL; AF092844; AAL40179.1; -.

DR HSP; Q9UMT8; 1YCR.

DR GO; GO:0005730; C:nucleolus; ISS.

DR GO; GO:0005654; C:nucleoplasm; ISS.

DR GO; GO:0017163; P:negative regulator of basal transcription a. . .; ISS.

DR GO; GO:0005515; F:protein binding; ISS.

DR GO; GO:0000122; P:negative regulation of transcription from P. . .; ISS.

DR InterPro; IPR010984; MDM2.

DR InterPro; IPR003121; SWIB MDM2.

DR InterPro; IPR001876; Znf\_RanGDP.

DR InterPro; IPR001841; Znf\_Ring.

DR Pfam; PF02201; SWIB; 1.

DR Pfam; PF00641; zf-RanBP; 1.

DR SMART; SM00184; RING; 1.





SEQUENCE FROM A.T.T.  
STRAIN=C57BL/6; TISSUE=Mouse;

[illegible]

	Query Match	78.2%;	Score 433.5;	DB 1;	Length 466;
	Best Local Similarity	81.7%;	Pred. No. 8.2e-35;		
	Matches	89;	Conservative	7;	Mismatches 12;
				Indels	1; Gaps 1;
QY	1	SOIPASEQETKVRPDKLLKLLKSKYGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHV	60		
DB	9	SOIPASEQETKVRPDKFLKLLKSKYGAQKDTYTMKEII-LSWQYIMTKRLYDEKQOHV	67		
QY	61	CSNDKLGDLGVKYSFVKEHRKIYIMVIRNLVNVNQSSDSGTGSVEN	109		

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:54:26 ; Search time 22.2 Seconds  
(without alignments)  
325.615 Million cell updates/sec

Title: US-10-822-254-12  
Perfect score: 554  
Sequence: 1 SQIPASEQETKVRPKPLK.....NLVVNQESSDSTSVSEN 109

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_AA\*  
1: /cgm2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgm2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgm2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgm2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgm2\_6/ptodata/1/iaa/PTCUS\_COMB.pep:\*  
6: /cgm2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	511	92.2	188	4	US-09-603-052-4
2	511	92.2	491	1	US-07-903-103-2
3	511	92.2	491	1	US-08-044-619A-2
4	511	92.2	491	1	US-08-283-911-2
5	511	92.2	491	1	US-08-245-500A-3
6	511	92.2	491	1	US-08-390-546-3
7	511	92.2	491	1	US-08-390-479A-3
8	511	92.2	491	1	US-08-557-393-3
9	511	92.2	491	1	US-08-390-516C-3
10	511	92.2	491	1	US-08-390-517A-3
11	511	92.2	491	1	US-08-390-515A-3
12	511	92.2	491	2	US-08-801-718-3
13	511	92.2	491	3	US-09-170-159A-3
14	511	92.2	491	4	US-09-480-718-44
15	494.5	89.3	216	3	US-09-510-252-4
16	451.5	81.5	489	1	US-07-903-103-4
17	451.5	81.5	489	1	US-08-044-619A-4
18	451.5	81.5	489	1	US-08-283-911-4
19	451.5	81.5	489	1	US-08-245-500A-5
20	451.5	81.5	489	1	US-08-390-546-5
21	451.5	81.5	489	1	US-08-390-479A-5
22	451.5	81.5	489	1	US-08-557-393-5
23	451.5	81.5	489	1	US-08-390-516C-5
24	451.5	81.5	489	1	US-08-390-517A-5
25	451.5	81.5	489	1	US-08-390-515A-5
26	451.5	81.5	489	2	US-08-801-718-5
27	451.5	81.5	489	3	US-09-170-159A-5

28	451.5	81.5	489	4	US-09-480-718-46	Sequence 46, Appl
29	164	29.6	243	4	US-09-786-702-2	Sequence 2, Appl
30	68.5	12.4	505	4	US-09-252-991A-29343	Sequence 29343, A
31	68	12.3	1432	3	US-08-781-891-71	Sequence 71, Appl
32	68	12.3	1432	3	US-09-618-166-71	Sequence 71, Appl
33	67.5	12.2	244	4	US-09-543-681A-6675	Sequence 6675, Ap
34	67	12.1	206	3	US-09-311-311C-22	Sequence 22, Appl
35	67	12.1	418	1	US-08-224-930-4	Sequence 4, Appl
36	67	12.1	418	3	US-08-908-436-6	Sequence 6, Appl
37	67	12.1	418	3	US-09-561-756-18	Sequence 18, Appl
38	67	12.1	418	3	US-09-227-721-18	Sequence 18, Appl
39	67	12.1	418	4	US-09-954-697-18	Sequence 18, Appl
40	66.5	12.0	198	3	US-09-213-293D-10	Sequence 10, Appl
41	66.5	12.0	550	4	US-09-075-505-7	Sequence 7, Appl
42	66.5	12.0	816	1	US-08-038-760-3	Sequence 3, Appl
43	66.5	12.0	816	2	US-08-470-091-3	Sequence 3, Appl
44	66.5	12.0	928	1	US-08-204-329-1	Sequence 1, Appl
45	66.5	12.0	928	2	US-08-959-638-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1  
US-09-603-052-4  
; Sequence 4, Application US/09603052  
; Patent No. 6492116  
; GENERAL INFORMATION:  
; APPLICANT: Chene, Patrick  
; APPLICANT: Hochkeppel, Heinz-Kurt  
; TITLE OF INVENTION: Assay for identifying inhibitors of the interaction  
; FILE REFERENCE: MEMB26.001C1  
; CURRENT APPLICATION NUMBER: US/09/603,052  
; CURRENT FILING DATE: 2000-06-26  
; PRIOR APPLICATION NUMBER: EP 95810576.9  
; PRIOR FILING DATE: 1995-09-18  
; PRIOR APPLICATION NUMBER: PCT/EP96/03957  
; PRIOR FILING DATE: 1996-09-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 188  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-603-052-4

Query Match 92.2%; Score 511; DB 4; Length 188;  
Best Local Similarity 94.5%; Pred. No. 9e-54;  
Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Oy 1 SQIPASEQETKVRPKPLKLLKLSVGAOKDTYTMKEVLHVLGQYIMTKRLYDEKQOHIVK 60  
Db 17 SQIPASEQETLVRPKPLLLKLSVGAOKDTYTMKEVLHVLGQYIMTKRLYDEKQOHIVY 76  
Oy 61 CSNDKGLDFGVGSPFSVKEHKIYTIYRNLVNVNQESSDSTSVSEN 109  
Db 77 CSNDLGLDFGVGSPFSVKEHKIYTIYRNLVNVNQESSDSTSVSEN 125

RESULT 2  
US-07-903-103-2  
; Sequence 2, Application US/07903103  
; Patent No. 5411860  
; GENERAL INFORMATION:  
; APPLICANT: VOGELSTEIN, BERT  
; APPLICANT: KINZLER, KENNETH  
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
; TITLE OF INVENTION: HUMAN TUMORS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
; STREET: 1001 G ST., N.W.

```
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/903.103
; FILING DATE: 19920623
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/867.840
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.40148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-903-103-2

Query Match          92.2%; Score 511; DB 1; Length 491;
Best Local Similarity 94.5%; Pred. No. 2.8e-53;
Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIVK 60
    |||||
DB 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDKLGDLFGVKSFSVKEHRKIYTMIRNLYVNVNQESSDSGTSVSEN 109
    |||||
DB 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLYVNVNQESSDSGTSVSEN 125

US-07-903-103-2

Query Match          92.2%; Score 511; DB 1; Length 491;
Best Local Similarity 94.5%; Pred. No. 2.8e-53;
Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIVK 60
    |||||
DB 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDKLGDLFGVKSFSVKEHRKIYTMIRNLYVNVNQESSDSGTSVSEN 109
    |||||
DB 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLYVNVNQESSDSGTSVSEN 125

US-08-044-619A-2

RESULT 3
US-08-044-619A-2
; Sequence 2, Application US/08044619A
; Patent No. 542063
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY
; APPLICANT: 720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G ST., N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/044,619A
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/903,103

; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/903.103
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.40148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-044-619A-2

Query Match          92.2%; Score 511; DB 1; Length 491;
Best Local Similarity 94.5%; Pred. No. 2.8e-53;
Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIVK 60
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DB 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDKLGDLFGVKSFSVKEHRKIYTMIRNLYVNVNQESSDSGTSVSEN 109
    |||||
DB 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLYVNVNQESSDSGTSVSEN 125

US-08-283-911-2

RESULT 4
US-08-283-911-2
; Sequence 2, Application US/08283911
; Patent No. 5519118
; GENERAL INFORMATION:
; APPLICANT: VOGELSTEIN, BERT
; APPLICANT: KINZLER, KENNETH
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G ST., N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/283,911
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/903,103
; FILING DATE: 23-JUN-1992
; APPLICATION NUMBER: US 07/867.840
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.40148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
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ADDRESSEE: BANNER & WITCOFF, LTD.  
STREET: 1001 G STREET, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,479A  
FILING DATE: 02-FEB-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: KAGAN, SARAH A.  
REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 01107.48992  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299  
TELEX: 197430 BMB UT  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 491 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-557-393-3  
Query Match 92.2%; Score 511; DB 1; Length 491;  
Best Local Similarity 94.5%; Pred. No. 2.8e-53;  
Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Qy 1 SQIPASEQETKVRPKPLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIVK 60  
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIVY 76  
Qy 61 CSNDKLGDLFGVKSFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 109  
Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 125  
RESULT 9  
US-08-390-516C-3  
Sequence 3, Application US/08390516C  
Patent No. 5708136  
GENERAL INFORMATION:  
APPLICANT: BURRELL, MARILEE  
APPLICANT: HILL, DAVID E.  
APPLICANT: KINZLER, KENNETH W.  
APPLICANT: VOGELSTEIN, BERT  
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
TITLE OF INVENTION: HUMAN TUMORS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
STREET: 1001 G STREET, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,516C  
FILING DATE: 07-APR-1993  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: KAGAN, SARAH A.  
REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 01107.42798  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299  
TELEX: 197430 BMB UT  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 491 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

ADDRESSEE: BANNER & WITCOFF, LTD.  
STREET: 1001 G STREET, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,479A  
FILING DATE: 02-FEB-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: KAGAN, SARAH A.  
REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 01107.48992  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299  
TELEX: 197430 BMB UT  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 491 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-390-479A-3  
Query Match 92.2%; Score 511; DB 1; Length 491;  
Best Local Similarity 94.5%; Pred. No. 2.8e-53;  
Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Qy 1 SQIPASEQETKVRPKPLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIVK 60  
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIVY 76  
Qy 61 CSNDKLGDLFGVKSFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 109  
Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 125  
RESULT 8  
US-08-557-393-3  
Sequence 3, Application US/08557393  
Patent No. 5702903  
GENERAL INFORMATION:  
APPLICANT: BURRELL, MARILEE  
APPLICANT: HILL, DAVID E.  
APPLICANT: KINZLER, KENNETH W.  
APPLICANT: VOGELSTEIN, BERT  
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
TITLE OF INVENTION: HUMAN TUMORS  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
STREET: 1001 G STREET, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/557,393  
FILING DATE: 13-NOV-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:



US-08-390-516C-3

Query Match 92.2%; Score 511; DB 1; Length 491;  
 Best Local Similarity 94.5%; Pred. No. 2.8e-53;  
 Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIYK 60  
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 Db 17 SQIPASEQETLVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIY 76  
 |||||

Qy 61 CSNDKLGDLFGVKSFSVKEHRKIYTMIRNVLVNVNQESSDSTSVSEN 109  
 |||||  
 Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNVLVNVNQESSDSTSVSEN 125  
 |||||

RESULT 10

US-08-390-517A-3  
 ; Sequence 3, Application US/08390517A  
 ; Patent No. 5736338  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BURRELL, MARILEE  
 ; APPLICANT: HILL, DAVID E.  
 ; APPLICANT: KINZLER, KENNETH W.  
 ; APPLICANT: VOGELSTEIN, BERT  
 ; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
 ; TITLE OF INVENTION: HUMAN TUMORS  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
 ; STREET: 1001 G STREET, N.W.  
 ; CITY: WASHINGTON  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20001  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/390,517A  
 ; FILING DATE: 07-APR-1993  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: KAGAN, SARAH A.  
 ; REGISTRATION NUMBER: 32,141  
 ; REFERENCE/DOCKET NUMBER: 01107.42798  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-508-9100  
 ; TELEFAX: 202-508-9299  
 ; TELEX: 197430 BBMB UT  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 491 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 US-08-390-517A-3

Query Match 92.2%; Score 511; DB 1; Length 491;  
 Best Local Similarity 94.5%; Pred. No. 2.8e-53;  
 Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIYK 60  
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 Db 17 SQIPASEQETLVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIY 76  
 |||||

Qy 61 CSNDKLGDLFGVKSFSVKEHRKIYTMIRNVLVNVNQESSDSTSVSEN 109  
 |||||  
 Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNVLVNVNQESSDSTSVSEN 125  
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RESULT 11

US-08-390-515A-3  
 ; Sequence 3, Application US/08390515A  
 ; Patent No. 5756455  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BURRELL, MARILEE  
 ; APPLICANT: HILL, DAVID E.  
 ; APPLICANT: KINZLER, KENNETH W.  
 ; APPLICANT: VOGELSTEIN, BERT  
 ; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
 ; TITLE OF INVENTION: HUMAN TUMORS  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
 ; STREET: 1001 G STREET, N.W.  
 ; CITY: WASHINGTON  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20001  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/390,515A  
 ; FILING DATE: 07-APR-1993  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: KAGAN, SARAH A.  
 ; REGISTRATION NUMBER: 32,141  
 ; REFERENCE/DOCKET NUMBER: 01107.42798  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-508-9100  
 ; TELEFAX: 202-508-9299  
 ; TELEX: 197430 BBMB UT  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 491 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 US-08-390-515A-3

Query Match 92.2%; Score 511; DB 1; Length 491;  
 Best Local Similarity 94.5%; Pred. No. 2.8e-53;  
 Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIYK 60  
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 Db 17 SQIPASEQETLVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIY 76  
 |||||

Qy 61 CSNDKLGDLFGVKSFSVKEHRKIYTMIRNVLVNVNQESSDSTSVSEN 109  
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RESULT 12

US-08-801-718-3  
 ; Sequence 3, Application US/08801718  
 ; Patent No. 5858976  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BURRELL, MARILEE  
 ; APPLICANT: HILL, DAVID E.  
 ; APPLICANT: KINZLER, KENNETH W.  
 ; APPLICANT: VOGELSTEIN, BERT  
 ; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
 ; TITLE OF INVENTION: HUMAN TUMORS  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
 ; STREET: 1001 G STREET, N.W.  
 ; CITY: WASHINGTON  
 ; STATE: D.C.

COUNTRY: USA  
ZIP: 20001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/801,718  
FILING DATE: 14-FEB-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/390,515  
FILING DATE: 07-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KAGAN, SARAH A.  
REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 01107.42798  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299  
TELEX: 197430 BEMB UT  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 491 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-801-718-3

Query Match 92.2%; Score 511; DB 2; Length 491;  
Best Local Similarity 94.5%; Pred. No. 2.8e-53;  
Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 SQIPASQETKVRPKPLKLLKSVGAQKDTYTMKEVLHVLGQYIMTKRLYDEKQOHIVK 60  
Db 17 SQIPASEQETLVRPKPLLLKLLSVGAQKDTYTMKEVLFLYLGQYIMTKRLYDEKQOHIVY 76  
QY 61 CSNDKLGDLGPFVKFSFVKHEHKIYTMIRNLVVVNQESSDSGTSVSEN 109  
Db 77 CSNDLLGDLGPFVKFSFVKHEHKIYTMIRNLVVVNQESSDSGTSVSEN 125

RESULT 13  
US-09-170-159A-3  
Sequence 3, Application US/09170159A  
Patent No. 6399755  
GENERAL INFORMATION:  
APPLICANT: BURRELL, MARLEE  
HILL, DAVID E.  
KINZLER, KENNETH W.  
VOGELSTEIN, BERT  
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
HUMAN TUMORS  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
STREET: 1001 G STREET, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/170,159A  
FILING DATE: 13-Oct-1998  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: KAGAN, SARAH A.

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; APPLICANT: CuraGen Corporation
; TITLE OF INVENTION: MDM INTERACTING PROTEIN AND METHODS OF USE THEREOF
; FILE REFERENCE: 15966-524 MDM US
; CURRENT APPLICATION NUMBER: US/09/510,252
; CURRENT FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: USN 60/121,192
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: USN 60/122,643
; PRIOR FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-510-252-4

Query Match      89.3%; Score 494.5; DB 3; Length 216;
Best Local Similarity 93.6%; Pred.No. 9.5e-52; Indels 1; Gaps 1;
Matches 102; Conservative 0; Mismatches 6;

Qy      1  SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHLYLGQYIMTKRLYDEKQQHIVK 60
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Qy      61  CSNDKLGDLFGVKSFSVKEHRKIYTMIRNLLVWVNNQSSDSGTSVSEN 109
Db      76  CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLLVWVNNQSSDSGTSVSEN 124

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Search completed: January 27, 2005, 18:17:08  
Job time : 23.2 secs

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RESULT 2  
US-09-956-425-8

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; Sequence 8, Application US/09956425
; Patent No. US20020045192A1
; GENERAL INFORMATION:
; APPLICANT: Kriwacki, Richard
; APPLICANT: Bothner, Brian
; APPLICANT: Lewis, William
; TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and Method of Use Thereof
; FILE REFERENCE: 1340/1/035
; CURRENT APPLICATION NUMBER: US/09/956,425
; CURRENT FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-956-425-8

Query Match          92.2%; Score 511; DB 9; Length 491;
Best Local Similarity 94.5%; Pred. No. 1.7e-47;
Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIVK 60
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDKLGDLFGVKSFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 109
Db 77 CSNDLLGDLFGVPSFVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 125

RESULT 3
US-09-029-327-2
; Sequence 2, Application US/09029327
; Publication No. US20030060432A1
; GENERAL INFORMATION:
; APPLICANT: TOCQUE, Bruno
; APPLICANT: WASLYK, Bohdan
; APPLICANT: DUBS-POTERSZMAN,
; APPLICANT: Marie-Christine
; TITLE OF INVENTION: ANTAGONISTS OF THE ONCOGENIC ACTIVITY OF
; TITLE OF INVENTION: THE PROTEIN MDM2, AND USE THEREOF IN THE TREATMENT OF
; TITLE OF INVENTION: CANCERS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, Mailstop 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/029,327
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 96/01340
; FILING DATE: 02-SEP-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO FR95/10331
; FILING DATE: 04-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fehlner Esq., Paul F.
; REGISTRATION NUMBER: 35,135
; REFERENCE/DOCKET NUMBER: ST95050-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-029-327-2

Query Match          92.2%; Score 511; DB 10; Length 491;
Best Local Similarity 94.5%; Pred. No. 1.7e-47;
Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIVK 60
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDKLGDLFGVKSFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 109
Db 77 CSNDLLGDLFGVPSFVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 125

RESULT 4
US-09-966-724-2
; Sequence 2, Application US/09966724
; Publication No. US20040170971A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: 720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G ST., N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/966,724
; FILING DATE: 01-Oct-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/044,619
; FILING DATE: 2001-10-01
; APPLICATION NUMBER: US 07/867,840
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.40148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-966-724-2

Query Match          92.2%; Score 511; DB 11; Length 491;
Best Local Similarity 94.5%; Pred. No. 1.7e-47;
Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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Qy	1	SOIPASEQETVPKPKLLKLLKLSVGAQKDTYTMKEVLHYLQYIMTKELYDEKQOHVK	60
Db	17	SOIPASEQETVPKPKLLKLLKLSVGAQKDTYTMKEVLHYLQYIMTKELYDEKQOHVY	76
Qy	61	CSNDKLGDLPFGVKSFVSKHKRTYTIMRYNLVVNQOESSDGTSTVSEN	109
Db	77	CSNDKLGDLPFGVKSFVSKHKRTYTIMRYNLVVNQOESSDGTSTVSEN	125

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RESULT 5
US-10-422-536-137
US-10-422-536-137
; Sequence 137, Application US/10422536
; Publication No. US20040014100A1
; GENERAL INFORMATION:
; APPLICANT: Kinsella, Todd
; APPLICANT: Lorens, James
; APPLICANT: Pray, Todd
; APPLICANT: Bennett, Mark
; TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR INHIBITING
; TITLE OF INVENTION: PROTEIN-PROTEIN INTERACTION
; FILE REFERENCE: A-71433-1/AMP/CYO
; CURRENT APPLICATION NUMBER: US/10/422,536
; CURRENT FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: US 60/187,130
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 09/800,770
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: US 10/232,758
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 137
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-422-536-137

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[illegible]

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RESULT 6
US-10-232-951-35
; Sequence 35, Application US/10232951
; Publication No. US20040043386A1
; GENERAL INFORMATION:
; APPLICANT: Pray, Todd
; APPLICANT: Wong, Brian
; APPLICANT: Bennett, Mark
; APPLICANT: Parlati, Francesco
; APPLICANT: Rigel Pharmaceuticals, Incorporated
; TITLE OF INVENTION: Methods and Compositions for Functional Ubiquitin
; TITLE OF INVENTION: Assays
; FILE REFERENCE: 021044-006800US
; CURRENT APPLICATION NUMBER: US/10/232,951
; CURRENT FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: E3 ubiquitin ligating agent mouse double minute 2

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; OTHER INFORMATION: (mdm2) homolog full length protein isoform, mouse
; OTHER INFORMATION: p53-binding protein (MDM2) homolog, transcript
; OTHER INFORMATION: variant MDM2, transformed 3T3 cell double minute 2,
; OTHER INFORMATION: Mdm2 CDNA
US-10-232-951-35

Query March          92.2%; Score 511; DB 15; Length 491;
Best Local Similarity 94.5%; Pred. No. 1.7e-47;
Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy  1  SQIPASQEYKVRPKPLLKLLKLSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
      |||||
Db   17  SQIPASQEETLVRPKPLLKLLKLSVGAQKDTYTMKEVLFGYQYIMTKRLYDEKQQHIVY 76
      |||||

Qy  61  CSNDKLGDLFGVKSFVSKEHRKITYMIYRNLVVMNQESSDSGTGSVSEN 109
      |||||

Db   77  CSNDLGLDGFVGPSFVSKEHRKITYMIYRNLVVMNQESSDSGTGSVSEN 125
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RESULT 7
US-10-685-838-1
; Sequence 1, Application US/10685838
; Publication No. US20040197893A1
; GENERAL INFORMATION:
; APPLICANT: SHUBERT, CARSTEN
; APPLICANT: GRASBERGER, BRUCE
; APPLICANT: MAGUIRE, DIANE
; APPLICANT: DECKMAN, INGRID
; APPLICANT: SPURLINO, JOHN
; TITLE OF INVENTION: HDM2-INHIBITOR COMPLEXES AND USES THEREOF
; FILE REFERENCE: PRD-2137-USANP
; CURRENT APPLICATION NUMBER: US/10/685,838
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: 60/418,350
; PRIOR FILING DATE: 2002-10-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-685-838-1

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Query Match	92.2%	Score 511;	DB 17;	Length 491;
Best Local Similarity	94.5%;	Pred. No. 1.7e-47;		
Matches 103;	Conservative 0;	Mismatches 6;	Indels 0;	Gaps 0;
Qy	1	SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHVK	60	
Db	17	SQIPASEQETLVRPKPLLKLLKSVGAQKDTYTMKEVLPYLGQYIMTKRLYDEKQOHIV	76	
Qy	61	CSNDKLGLDFGVKFSFVKHKRTYIMYRNLVVNNQOESSDSDGTSVSEN	109	
Db	77	CSNDLGLDIFGVPSFVKHKRTYIMYRNLVVNNQOESSDSDGTSVSEN	125	

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RESULT 8
US-10-724-225-2
; Sequence 2, Application US/10724225
; Publication No. US20040209834A1
; GENERAL INFORMATION:
; APPLICANT: TOCQUE, Bruno
; WASLYK, Bondan
; DUBS-POTERSZMAN,
; Marie-Christine
; TITLE OF INVENTION: ANTAGONISM
; OF THE PROTEIN
; CANCERS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc
; STREET: 500 Arcola Road
; CITY: Collegeville
;

```

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; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/724,225
; FILING DATE: 01-Dec-2003
; CLASSIFICATION: 514
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/09/029,327
; FILING DATE: <unknown>
; APPLICATION NUMBER: FR 96/01340
; FILING DATE: 02-SEP-1996
; APPLICATION NUMBER: WO FR95/10331
; FILING DATE: 04-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fehlnner Esq., Paul F.
; REGISTRATION NUMBER: 35,135
; REFERENCE/DOCKET NUMBER: ST95050-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-724-225-2

Query Match 92.2%; Score 511; DB 17; Length 491;
Best Local Similarity 94.5%; Pred. No. 1.7e-47;
Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 SQIPASEQETKVRPKPLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIVK 60
DB 17 SQIPASEQETLVRPKPLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDKLGDLFGVKSFVKEHRKIYTMIRNLVVVNQSSDSGTSVSEN 109
DB 77 CSNDLLGDLFGVPSPFVKEHRKIYTMIRNLVVVNQSSDSGTSVSEN 125

RESULT 9
US-10-489-802-8
; Sequence 8, Application US/10489802
; Publication No. US20040248198A1
; GENERAL INFORMATION:
; APPLICANT: St. Jude Children's Research Hospital, Inc.
; APPLICANT: Kriwacki, Richard
; APPLICANT: Bothner, Brian
; APPLICANT: Lewis, William
; TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and
; TITLE OF INVENTION: Method of Use Thereof
; FILE REFERENCE: 44158/243642
; CURRENT APPLICATION NUMBER: US/10/489,802
; CURRENT FILING DATE: 2004-03-16
; PRIOR APPLICATION NUMBER: US 09/956,425
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-489-802-8

Query Match 92.2%; Score 511; DB 17; Length 491;

; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/724,225
; FILING DATE: 01-Dec-2003
; CLASSIFICATION: 514
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/09/029,327
; FILING DATE: <unknown>
; APPLICATION NUMBER: FR 96/01340
; FILING DATE: 02-SEP-1996
; APPLICATION NUMBER: WO FR95/10331
; FILING DATE: 04-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fehlnner Esq., Paul F.
; REGISTRATION NUMBER: 35,135
; REFERENCE/DOCKET NUMBER: ST95050-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-723-860-2236

Query Match 92.2%; Score 511; DB 17; Length 491;
Best Local Similarity 94.5%; Pred. No. 1.7e-47;
Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 SQIPASEQETKVRPKPLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIVK 60
DB 17 SQIPASEQETLVRPKPLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDKLGDLFGVKSFVKEHRKIYTMIRNLVVVNQSSDSGTSVSEN 109
DB 77 CSNDLLGDLFGVPSPFVKEHRKIYTMIRNLVVVNQSSDSGTSVSEN 125

RESULT 10
US-10-723-860-2236
; Sequence 2236, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods for Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2236
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-2236

Query Match 92.2%; Score 511; DB 17; Length 491;
Best Local Similarity 94.5%; Pred. No. 1.7e-47;
Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 SQIPASEQETKVRPKPLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIVK 60
DB 17 SQIPASEQETLVRPKPLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDKLGDLFGVKSFVKEHRKIYTMIRNLVVVNQSSDSGTSVSEN 109
DB 77 CSNDLLGDLFGVPSPFVKEHRKIYTMIRNLVVVNQSSDSGTSVSEN 125

RESULT 11
US-10-057-510-4
; Sequence 4, Application US/10057510
; Publication No. US20020098580A1
; GENERAL INFORMATION:
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Yang, Meijia
; APPLICANT: Schulz, Vincent
; APPLICANT: CuraGen Corporation
; TITLE OF INVENTION: MDM INTERACTING PROTEIN AND METHODS OF USE THEREOF
; FILE REFERENCE: 15966-524 MDM US
; CURRENT APPLICATION NUMBER: US/10/057,510
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: USSN 09/510,252
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: USSN 60/121,192
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: USSN 60/122,643
; PRIOR FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-057-510-4
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APPLICANT: Vernet, Corine A.M.,  
APPLICANT: Zehrusen, Bryan D.,  
APPLICANT: Zhong, Mei  
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
FILE REFERENCE: 21402-480C  
CURRENT APPLICATION NUMBER: US/10/287,226  
CURRENT FILING DATE: 2002-11-04  
PRIORITY APPLICATION NUMBER: 60/334,421  
PRIORITY FILING DATE: 2001-11-30  
PRIORITY APPLICATION NUMBER: 60/354,392  
PRIORITY FILING DATE: 2002-02-04  
PRIORITY APPLICATION NUMBER: 60/360,148  
PRIORITY FILING DATE: 2002-02-27  
PRIORITY APPLICATION NUMBER: 60/364,000  
PRIORITY FILING DATE: 2002-03-13  
PRIORITY APPLICATION NUMBER: 60/404,821  
PRIORITY FILING DATE: 2002-08-20  
PRIORITY APPLICATION NUMBER: 60/334,526  
PRIORITY FILING DATE: 2001-11-30  
PRIORITY APPLICATION NUMBER: 60/354,409  
PRIORITY FILING DATE: 2002-02-04  
PRIORITY APPLICATION NUMBER: 60/364,227  
PRIORITY FILING DATE: 2002-03-13  
PRIORITY APPLICATION NUMBER: 60/334,027  
PRIORITY FILING DATE: 2001-11-28  
PRIORITY APPLICATION NUMBER: 60/331,641  
PRIORITY FILING DATE: 2001-11-20  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 673  
SOFTWARE: CuraseqList version 0.1  
SEQ ID NO 382  
LENGTH: 522  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-287-226-382

Query Match 87.6%; Score 485.5; DB 15; Length 522;  
Best Local Similarity 73.6%; Pred. No. 1.2e-44;  
Matches 103; Conservative 0; Mismatches 6; Indels 31; Gaps 1;  
QY 1 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKE-----36  
DB 17 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEFTMLPRLVWNSWAQICLPRP 76  
QY 37 -----VLHYLGQYIMTKRLYDEKQKHVKSNDKLGDLFGVKFSVKEHRKIYTMIR 89  
DB 77 PKVLDQLVFLYGLQYIMTKRLYDEKQKHVYCSNDLLGLDGLFGVPSVKEHRKIYTMIR 136  
QY 90 NLVVVNQESSDSGTSVSEN 109  
DB 137 NLVVVNQESSDSGTSVSEN 156

RESULT 14  
US-09-956-425-6  
Sequence 6, Application US/09956425  
Patent No. US2002045192A1  
GENERAL INFORMATION:  
APPLICANT: Kriwacki, Richard  
APPLICANT: Bothner, Brian  
APPLICANT: Lewis, William  
TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and Method of Use Thereof  
FILE REFERENCE: 1340/1/035  
CURRENT APPLICATION NUMBER: US/09/956,425  
CURRENT FILING DATE: 2001-09-19  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 6  
LENGTH: 489  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-956-425-6

Query Match 81.5%; Score 451.5; DB 9; Length 489;  
Best Local Similarity 82.6%; Pred. No. 5.9e-41;  
Matches 90; Conservative 7; Mismatches 9; Indels 3; Gaps 1;  
QY 1 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQKHV 60  
DB 17 SQIPASEQETLVPRPKLLKLLKSVGAQNDYTMKEIIFYIGQYIMTKRLYDEKQKHV 76  
QY 61 CSNDKLGDLFGVKFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 109  
DB 77 CSNDLLGDVFGVPSVKEHRKIYMIYRNLVAVSQ---DSGTSLSSES 122

RESULT 15  
US-09-966-724-4  
Sequence 4, Application US/09966724  
Publication No. US20040170971A1  
GENERAL INFORMATION:  
APPLICANT: THE JOHNS HOPKINS UNIVERSITY  
720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA  
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
HUMAN TUMORS  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
STREET: 1001 G ST., N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20001-4597  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/966,724  
FILING DATE: 01-Oct-2001  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/044,619  
FILING DATE: 2001-10-01  
APPLICATION NUMBER: US 07/867,840  
FILING DATE: 07-APR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: KAGAN, SARAH A.  
REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 01107.40148  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299  
TELEX: 197430 BBMB UT  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 489 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-966-724-4

Query Match 81.5%; Score 451.5; DB 11; Length 489;  
Best Local Similarity 82.6%; Pred. No. 5.9e-41;  
Matches 90; Conservative 7; Mismatches 9; Indels 3; Gaps 1;  
QY 1 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQKHV 60  
DB 17 SQIPASEQETLVPRPKLLKLLKSVGAQNDYTMKEIIFYIGQYIMTKRLYDEKQKHV 76  
QY 61 CSNDKLGDLFGVKFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 109  
DB 77 CSNDLLGDVFGVPSVKEHRKIYMIYRNLVAVSQ---DSGTSLSSES 122

Search completed: January 27, 2005, 18:23:07  
Job time : 70.4 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:52:56 ; Search time 19.8 Seconds  
(without alignments)  
529.678 Million cell updates/sec

Title: US-10-822-254-8  
Perfect score: 554  
Sequence: 1 SQIPASQETLVRPKPLLLK.....NLVVNQESSDSGTSVSEN 109  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	550	99.3	491	1 S24354	p53-binding protein
2	490.5	88.5	489	2 S15349	mdm2-protein
3	279.5	50.5	489	2 S71955	MDM2-like p53-bind
4	77	13.9	685	1 SXBPT4	NAD+-protein ADP-r
5	77	13.9	698	1 S31630	NAD+-protein ADP-r
6	77	13.9	698	1 S31714	NAD+-protein ADP-r
7	76	13.7	967	2 A64710	type III restricti
8	72.5	13.1	565	2 S52682	hypothetical prote
9	72	13.0	969	2 E71810	hypothetical prote
10	71.5	12.9	401	2 F90288	hypothetical prote
11	71.5	12.9	422	2 T26334	hypothetical prote
12	71.5	12.9	514	2 D85069	hypothetical prote
13	71	12.8	206	1 XUBYMC	methylated-DNA-lpr
14	70.5	12.7	838	2 I45557	eyeless, long form
15	69.5	12.5	331	2 B94938	flagellar motor sw
16	69	12.5	181	2 S75415	probable ribosomal
17	68.5	12.4	277	2 A10589	conserved hypothet
18	68.5	12.4	339	2 A90395	conserved hypothet
19	68	12.3	848	2 E86443	probable G-protein
20	68	12.3	860	2 S64366	exodeoxyribonuclea
21	67.5	12.2	517	2 S32169	hypothetical prote
22	67.5	12.2	709	2 E64213	DNA topoisomerase
23	67.5	12.2	1368	2 T18371	probable glutamate
24	67	12.1	170	2 T31967	hypothetical prote
25	67	12.1	261	2 H71680	exodeoxyribonuclea
26	67	12.1	1145	2 S55600	single-stranded DN
27	66.5	12.0	315	2 H81704	dipeptidase, proba
28	66.5	12.0	593	2 E81277	hypothetical prote
29	66.5	12.0	649	2 C81275	hypothetical prote

30	66.5	12.0	891	2 S27029	preprotein translo
31	66.5	12.0	1292	2 F64237	DNA-directed RNA p
32	66.5	12.0	2833	2 A43360	inositol 1,4,5-tri
33	66	11.9	1098	2 S38100	hypothetical prote
34	65.5	11.8	422	2 B95001	conserved domain p
35	65.5	11.8	445	2 A97873	conserved hypothet
36	65.5	11.8	447	2 I64002	sodium-translocati
37	65.5	11.8	455	2 S56695	1-aminocyclopropan
38	65.5	11.8	1268	2 T50252	probable transcrip
39	65	11.7	369	2 B70220	conserved hypothet
40	65	11.7	3092	2 S46009	GTPase-activating
41	65	11.7	3268	2 S69625	hypothetical prote
42	64.5	11.6	317	2 F97701	hypothetical prote
43	64.5	11.6	380	2 T32112	hypothetical prote
44	64.5	11.6	467	2 T25848	hypothetical prote
45	64.5	11.6	485	1 S19677	1-aminocyclopropan

## ALIGNMENTS

### RESULT 1

S24354

p53-binding protein mdm2 - human

N:Alternate names: mdm-2 oncogene; mouse double minute 2 homolog; p53-associated phospho

C:Species: Homo sapiens (man)

C:Date: 17-Mar-2000 #sequence revision 17-Mar-2000 #text\_change 17-Mar-2000

C:Accession: S24354; S57338; G02026

→ R:Oliner, J.D.; Kinzler, K.W.; Meltzer, P.S.; George, D.L.; Vogelstein, B.

Nature 358, 80-83, 1992

← Article: Amplification of a gene encoding a p53-associated protein in human sarcomas.

A:Reference number: S24354; MUID:92310576; PMID:1614537

A:Accession: S24354

A:Molecule type: mRNA

A:Residues: 1-491 <OLI>

A:Cross-references: EMBL:Z12020; NID:G35211; PIDN:CAA78055.1; PID:G35212

R:Zauberman, A.; Flusberg, D.; Haupt, Y.; Barak, Y.; Oren, M.

Nucleic Acids Res. 23, 2584-2592, 1995

← Article: A functional p53-responsive intronic promoter is contained within the human mdm

A:Reference number: S57338; MUID:95380270; PMID:7651818

A:Accession: S57338

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-16, 'P', 18-24 <ZAU>

A:Cross-references: EMBL:U28935; NID:G904033; PIDN:AAA82237.1; PID:G904034

R:Lunec, J.

submitted to the EMBL Data Library, August 1995

A:Description: Multiple alternate spliced mdm2 transcripts with loss of p53 binding doma

A:Reference number: G09070

A:Accession: G02026

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-27,223-491 <LUN>

A:Cross-references: EMBL:U31199; NID:G992676; PIDN:AAA75514.1; PID:G992677

A:Experimental source: splice form A

C:Genetics:

A:Gene: GDB:MDM2

A:Cross-references: GDB:250456; OMIM:164785

A:Map position: 12q14.3-12q15

C:Superfamily: human p53-binding protein mdm2

C:Keywords: alternative splicing; oncogene; phosphoprotein

F:1-491/Product: p53-binding protein mdm-2 #status predicted <MAT1>

F:1-27,223-491/Product: p53-binding protein mdm-2, splice form A #status predicted <MAT2>

Query Match 99.3%; Score 550; DB 1; Length 491;

Best Local Similarity 99.1%; Pred. No. 1.7e-48;

Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASQETLVRPKPLLLKLSVGAQKQTYTWKVELYVLGQYIMTKRLYDEKQOHIVY 60

Db 17 SQIPASQETLVRPKPLLLKLSVGAQKQTYTWKVELYVLGQYIMTKRLYDEKQOHIVY 76

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Qy 61 CSNDLLGDLFGVPSFVKHKKIYIMYRNLVVWVWQESSDGSSTSVSEN 109
|||||
Db 77 CSNDLLGDLFGVPSFVKHKKIYIMYRNLVVWVWQESSDGSSTSVSEN 125
|||||

RESULT 2
S15349
mdm2 protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S15349
R:Fakhrazadeh, S.S.; Trusko, S.P.; George, D.L.
EMBO J. 10, 1565-1569, 1991
A:Title: Tumorigenic potential associated with enhanced expression of a gene that is amp
A:Reference number: S15349; MUID:91224107; PMID:2026149
A:Accession: S15349
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-489 <FAK>
A:Cross-references: UNIPROT:P23804; EMBL:X58876; NID:g53038; PIDN:CAA41684.1; PID:g53039
C:Genetics:
C:Gene: mdm2
C:Superfamily: human p53-binding protein mdm2

Query Match 88.5%; Score 490.5; DB 2; Length 489;
Best Local Similarity 87.2%; Pred. No. 2.1e-42;
Matches 95; Conservative 8; Mismatches 3; Indels 3; Gaps 1;

Qy 1 SQIPASEQETLVRPKLLKLLKSVGAQDVTYMKVELVYLGOYIMTKRLYDEKQOHIVY 60
|||||
Db 17 SQIPASEQETLVRPKLLKLLKSVGAQDVTYMKELIIFYIQYIMTKRLYDEKQOHIVY 76
|||||

Qy 61 CSNDLLGDLFGVPSFVKHKKIYIMYRNLVVWVWQESSDGSSTSVSEN 109
|||||
Db 77 CSNDLLGDLFGVPSFVKHKKIYIMYRNLVVWVWQESSDGSSTSVSEN 122
|||||

RESULT 3
S17195
MDM2-like p53-binding protein MDMX - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
C:Accession: S17195
R:Shvarts, A.; Steegenga, W.T.; Riteco, N.; van Laar, T.; Dekker, P.; Bazuine, M.; van H
EMBO J. 15, 5349-5357, 1996
A:Title: MDMX: a novel p53-binding protein with some functional properties of MDM2.
A:Reference number: S17195; MUID:97050840; PMID:8895579
A:Accession: S17195
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-489 <SHV>
A:Cross-references: UNIPROT:Q35618; EMBL:AF007110; NID:g2253388; PIDN:AAB62927.1; PID:g2
C:Genetics:
C:Gene: MDMX
C:Function:
A:Description: inhibits transcription activation function of tumour suppressor protein p
C:Superfamily: human p53-binding protein mdm2

Query Match 50.5%; Score 279.5; DB 2; Length 489;
Best Local Similarity 53.3%; Pred. No. 8.1e-21;
Matches 56; Conservative 17; Mismatches 21; Indels 11; Gaps 1;

Qy 5 ASQEOTLVRPKLLKLLKSVGAQDVTYMKVELVYLGOYIMTKRLYDEKQOHIVYCSND 64
|||||
Db 20 SSEQISQVRPKQLLLKLLHAAGAQQEVFTMKVHVLGYIMVKQYDQEQEHMVYCGSD 79
|||||

Qy 65 LLGDLFGVPSFVKHKKIYIMYRNLVVWVWQESSDGSSTSVSEN 109
|||||
Db 80 LLGDLGCGQSFVKDPSPLYDMLRKNLV-----TSANN 113
|||||

RESULT 4
SXBPT4
```

```
NAD+-protein ADP-ribosyltransferase (EC 2.4.2.-) precursor - phase T4
C:Species: phage T4
A:Note: host Escherichia coli
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C:Accession: JU0096
R:Hilse, D.; Koch, T.; Rueger, W.
Nucleic Acids Res. 17, 6731, 1989
A:Title: Nucleotide sequence of the alt gene of bacteriophage T4.
A:Reference number: JU0096; MUID:89386005; PMID:2506526
A:Accession: JU0096
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-685 <HIL>
A:Cross-references: UNIPROT:P12726
C:Comment: This enzyme catalyzes the ADP-ribosylation of one of the two alpha-subunits c
C:Genetics:
C:Gene: alt
C:Superfamily: phage T4 NAD-protein ADP-ribosyltransferase
C:Keywords: glycosyltransferase; pentosyltransferase
F:7-685/Product: NAD-protein ADP-ribosyltransferase #status predicted <MAT>

Query Match 13.9%; Score 77; DB 1; Length 685;
Best Local Similarity 28.0%; Pred. No. 6.2;
Matches 28; Conservative 23; Mismatches 35; Indels 14; Gaps 6;

Qy 18 LLKLKLS--VGAQKDVTYMKVELVYL---GOYIMTKRL--YDEKQOH--VYCSNDLLGDL 69
|||||
Db 111 MLRLKSKTAGAQRQIQVIADRLIRSRGGRVLLKELWDYDKYAYILIHKNVSLDI 170
|||||

Qy 70 FGVPFSFVKHKKIYIMYRNLVVWVWQESSDGSSTSVSEN 109
|||||
Db 171 FGVPFISTELFTKVESKV--GDVYINK-----DTGAQVTKN 204
|||||

RESULT 5
S31630
NAD+-protein ADP-ribosyltransferase (EC 2.4.2.-) precursor - phase T2
C:Species: phage T2
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S31630
R:Koch, T.; Rueger, W.
submitted to the EMBL Data Library, December 1992
A:Description: The ADP-ribosyltransferase of bacteriophages T2, T4 and T6: Sequencing of
A:Reference number: S31630
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-698 <KOC>
A:Cross-references: UNIPROT:Q38424; EMBL:X69893; NID:gl5187; PIDN:CAA49517.1; PID:gl5188
C:Superfamily: phage T4 NAD-protein ADP-ribosyltransferase
C:Keywords: glycosyltransferase; NAD; pentosyltransferase

Query Match 13.9%; Score 77; DB 1; Length 698;
Best Local Similarity 28.0%; Pred. No. 6.4;
Matches 28; Conservative 23; Mismatches 35; Indels 14; Gaps 6;

Qy 18 LLKLKLS--VGAQKDVTYMKVELVYL---GOYIMTKRL--YDEKQOH--VYCSNDLLGDL 69
|||||
Db 112 MLRLKSKTAGAQRQIQVIADRLIRSRGGRVLLKELWDYDKYAYILIHKNVSLDI 171
|||||

Qy 70 FGVPFSFVKHKKIYIMYRNLVVWVWQESSDGSSTSVSEN 109
|||||
Db 172 FGVPFISTELFTKVESKV--GDVYINK-----DTGAQVTKN 205
|||||

RESULT 6
S31714
NAD+-protein ADP-ribosyltransferase (EC 2.4.2.-) precursor - phase T6
C:Species: phage T6
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S31714
R:Koch, T.; Rueger, W.
submitted to the EMBL Data Library, December 1992
```

A;Description: The ADP-ribosyltransferase of bacteriophages T2, T4 and T6: Sequencing of  
A;Reference number: S31630  
A;Accession: S31714  
A>Status: Preliminary  
A:Molecule type: DNA  
A;Residues: 1-698 <KOC>  
A;Cross-references: UNIPROT:Q38433; EMBL:X69894; NID:g15422; PIDN:CAA49518.1; PID:g15423  
C;Superfamily: phage T4 NAD-protein ADP-ribose transferase  
C;Keywords: glycosyltransferase; NAD; pentosyltransferase

Query Match 13.9%; Score 77; DB 1; Length 698;  
Best Local Similarity 28.0%; Pred. No. 6.4; Mismatches 23; Indels 14; Gaps 6;  
Matches 28; Conservative 23;

Qy 18 LLKLKLS--VGAQKDYTMKEVLYL---GOYIMTKRL--YDEKQOH-VYCSNDLLGDL 69  
: : | | | : : : : : | | | : : | : : | :  
Db 112 MLRIKSKTAGAQAIQVIADRLIRSSGGRYVLKKELWYDKYAILHRKNVSLEDI 171  
: : | | | : : : : : | | | : : | : : | :  
Qy 70 FGVPFSFKGHRKIYTYMYRNLVVVNQQESSDGSQTSVSEN 109  
| | | : : : : : | : : | : : | : : | :  
Db 172 PGVPEISTEITFTKVESKV--GDVYINK---DTGAQVTKN 205  
| | | : : : : : | : : | : : | : : | :

RESULT 7  
A64710  
type III restriction enzyme R protein - Helicobacter pylori (strain 26695)  
C;Species: Helicobacter pylori  
C;Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 09-Jul-2004  
C;Accession: A64710  
R;tomb, J.F.; White, O.; Kervlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.; Nature 388, 539-547, 1997  
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.  
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.  
A;Reference number: A64520; MUID:9739467; PMID:9252185  
A;Accession: A64710  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A;Residues: 1-967 <TOM>  
A;Cross-references: UNIPROT:O26050; GB:AEO00650; GB:AEO00511; NID:g2314700; PIDN:AAD0856  
C;Genetics:  
A;Start codon: GTG

Query Match 13.7%; Score 76; DB 2; Length 967;  
Best Local Similarity 24.8%; Pred. No. 12; Mismatches 43; Indels 14; Gaps 3;  
Matches 26; Conservative 22;

Qy 1 SQIPASEQETLVAPKPKLLKLSVGAQKDYTMKEVLYYIGQYIMTKR---LYDEKQOH 57  
: : | | | : : | | : : | : : | : : | : : | : :  
Db 768 NEIKKNEQEGLRULELFLEIIYNQIKDKISQWRETT-----IKNRKDAFYDEKGEI 821  
: : | | | : : | | : : | : : | : : | : : | : :  
Qy 58 IVYCSDNLLGLDGFVPSFVKHKKIYTYMYRNLVVVNQQESSDS 102  
: : | | | : : | | : : | : : | : : | : : | : :  
Db 822 REFLDGSLGADKVEIKNSSVRE----KCLYENFMQVDSEIEKXT 861  
: : | | | : : | | : : | : : | : : | : : | : :

RESULT 8  
S52682  
hypothetical protein YDR117c - yeast (Saccharomyces cerevisiae)  
N;Alternate names: hypothetical protein YD9727.12C  
C;Species: Saccharomyces cerevisiae  
C;Date: 19-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 09-Jul-2004  
C;Accession: S52682  
R;Murphy, L.; Shore, L.; Harris, D.  
submitted to the EMBL Data Library, March 1995  
A;Reference number: S52671  
A;Accession: S52682  
A:Molecule type: DNA  
A;Residues: 1-565 <MUR>  
A;Cross-references: UNIPROT:Q04600; EMBL:Z48758; NID:g747879; PID:g747891; GSPDB:GN00004  
C;Genetics:  
A;Gene: MIPS:YDR117c





Query Match 12.8%; Score 71; DB 1; Length 206;  
 Best Local Similarity 41.0%; Pred. No. 6.5;  
 Matches 25; Conservative 10; Mismatches 16; Indels 10; Gaps 4;  
 QY 33 TWKEVLYLQGVIMTK-----RLYDEKQOHIVYCS--NDLLGLDFGVPSFVKEHRKIYT 85  
 DB 18 TWKELLY--TFIEVTGAFVLFREKTNQVNFASLGNLKLFLGKVEGF-LKKHEKQDT 74  
 QY 86 M 86  
 DB 75 M 75  
 RESULT 14  
 I45557  
 eyeless, long form - fruit fly (Drosophila melanogaster)  
 C:Species: Drosophila melanogaster  
 C:Date: 09-Mar-1996 #sequence\_revision 09-Mar-1996 #text\_change 16-Aug-2004  
 C:Accession: I45557  
 R:Quiring, R.; Wallendorf, U.; Kloter, U.; Gehring, W.J.  
 Science 265, 785-789, 1994  
 A:Title: Homology of the eyeless gene of Drosophila to the Small eye gene in mice and A  
 A:Reference number: A54584; MUID:94323757; PMID:7914031  
 A:Accession: I45557  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-838 <RES>  
 A:Cross-references: EMBL:X79493; NID:G641809; PIDN:CAA56038.1; PID:G641810  
 C:Genetics:  
 A:Gene: FlyBase:ey  
 A:Cross-references: FlyBase:FBgn0005558  
 A:Introns: 37/1; 92/2; 152/3; 371/1; 429/1; 521/1; 639/2  
 C:Superfamily: homeobox homology; paired box homology  
 C:Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regulati  
 F:37-161/Domain: paired box homology <PBH>  
 F:412-468/Domain: homeobox homology <HOX>

Query Match 12.7%; Score 70.5; DB 2; Length 838;  
 Best Local Similarity 26.0%; Pred. No. 36;  
 Matches 26; Conservative 14; Mismatches 33; Indels 27; Gaps 5;  
 QY 12 VRPELLLLKLVCAQKDTYTMKEVLYLQY-----IMTKRLYDEKQOHIVYCSNDL 65  
 DB 99 IRP-----RAIGGSRVATAEVSQIKRECPISFAWEIRDLQENV-CTND- 148  
 QY 66 LGDLFGVPFVKEHRKIYTMIRNLVVVNQOESSDSGTS 105  
 DB 149 -----NIFSVS-----SINRVLRNLAAQKEQQSGSGSS 177  
 RESULT 15  
 B84938  
 flagellar motor switch protein flig [imported] - Buchnera sp. (strain APS)  
 C:Species: Buchnera sp.  
 C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 24-Aug-2001  
 C:Accession: B84938  
 R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.  
 Nature 407, 81-86, 2000  
 A:Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A  
 A:Reference number: A84930; MUID:20445173; PMID:10993077  
 A:Accession: B84938  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-331 <STO>  
 A:Cross-references: GB:AF000398; GSPDB:GN00144  
 A:Experimental source: strain APS  
 C:Genetics:  
 A:Gene: flig; BU074  
 C:Superfamily: flagellar switch protein flig  
 Query Match 12.5%; Score 69.5; DB 2; Length 331;  
 Best Local Similarity 26.4%; Pred. No. 16;

Matches 23; Conservative 16; Mismatches 31; Indels 17; Gaps 2;  
 QY 15 KPLLKLLKLVCAQKDTYTMKEVLYLQYIMTKRLYDEKQOHIVYCSNDLLGLDFGVPS 74  
 DB 75 KYLIKMLTKALGEKKGTSLLKEALEIRNARICIKALNYMKAKQVAFLLD----- 123  
 QY 75 FSVKEHRKIYTMIRNLVVVNQOESSD 101  
 DB 124 ---KEHPQIITTI---LICLNKNQSAE 144

Search completed: January 27, 2005, 18:15:10  
 Job time : 20.8 secs

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```
; Sequence 8, Application US/09956425
; Patent No. US20020045192A1
; GENERAL INFORMATION:
; APPLICANT: Kriwacki, Richard
; APPLICANT: Bothner, Brian
; APPLICANT: Lewis, William
; TITLE OF INVENTION: Axf and Hdm2 Interaction Domains and Method of Use Thereof
; FILE REFERENCE: 1340/1/035
; CURRENT APPLICATION NUMBER: US/09/956,425
; CURRENT FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-956-425-8

Query Match          99.3%; Score 550; DB 9; Length 491;
Best Local Similarity 99.1%; Pred. No. 1.4e-56;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLYLGYQYIMTKRLYDEKQHHIVY 60
Db      17 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLYLGYQYIMTKRLYDEKQHHIVY 76

Qy      61 CSNDLLGDLFGVPSPSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 109
Db      77 CSNDLLGDLFGVPSPSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 125

RESULT 3
US-09-029-327-2
; Sequence 2, Application US/09029327
; Publication No. US20030060432A1
; GENERAL INFORMATION:
; APPLICANT: TOCQUE, Bruno
; APPLICANT: WASYLK, Bohdan
; APPLICANT: DUBS-POTERSZMAN,
; APPLICANT: Marie-Christine
; TITLE OF INVENTION: THE ANTAGONISTS OF THE ONCOGENIC ACTIVITY OF
; TITLE OF INVENTION: THE PROTEIN MDM2, AND USE THEREOF IN THE TREATMENT OF
; TITLE OF INVENTION: CANCERS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, Mailstop 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/029,327
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 96/01340
; FILING DATE: 02-SEP-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO FR95/10331
; FILING DATE: 04-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fehlner Esq., Paul F.
; REGISTRATION NUMBER: 35,135
; REFERENCE/DOCKET NUMBER: ST95050-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-029-327-2

Query Match          99.3%; Score 550; DB 10; Length 491;
Best Local Similarity 99.1%; Pred. No. 1.4e-56;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLYLGYQYIMTKRLYDEKQHHIVY 60
Db      17 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLYLGYQYIMTKRLYDEKQHHIVY 76

Qy      61 CSNDLLGDLFGVPSPSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 109
Db      77 CSNDLLGDLFGVPSPSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 125

RESULT 4
US-09-966-724-2
; Sequence 2, Application US/09966724
; Publication No. US20040170971A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: 720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G ST., N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/966,724
; FILING DATE: 01-Oct-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/044,619
; FILING DATE: 2001-10-01
; APPLICATION NUMBER: US 07/867,840
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.40148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-966-724-2

Query Match          99.3%; Score 550; DB 11; Length 491;
Best Local Similarity 99.1%; Pred. No. 1.4e-56;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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STATE: PA  
COUNTRY: USA  
ZIP: 19426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/724,225  
FILING DATE: 01-Dec-2003  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/029,327  
FILING DATE: <unknown>  
APPLICATION NUMBER: FR 96/01340  
FILING DATE: 02-SEP-1996  
APPLICATION NUMBER: WO FR95/10331  
FILING DATE: 04-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Fehlnher Esq., Paul F.  
REGISTRATION NUMBER: 35,135  
REFERENCE/DOCKET NUMBER: ST95050-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 454-3839  
TELEFAX: (610) 454-3808  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 491 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-724-225-2

Query Match 99.3%; Score 550; DB 17; Length 491;  
Best Local Similarity 99.1%; Pred. No. 1.4e-56;  
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SQIPASQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVY 60  
DB 17 SQIPASQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVY 76  
QY 61 CSNDLLGDLFGVPFSVKHRKIYTMIRNLVVNQESSDSGTSVSEN 109  
DB 77 CSNDLLGDLFGVPFSVKHRKIYTMIRNLVVNQESSDSGTSVSEN 125

RESULT 9  
US-10-489-802-8  
Sequence 8, Application US/10489802  
Publication No. US20040248198A1  
GENERAL INFORMATION:  
APPLICANT: St. Jude Children's Research Hospital, Inc.  
APPLICANT: Kriwacki, Richard  
APPLICANT: Bothner, Brian  
APPLICANT: Lewis, William  
TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and  
TITLE OF INVENTION: Method of Use Thereof  
FILE REFERENCE: 44158/243642  
CURRENT APPLICATION NUMBER: US/10/489,802  
CURRENT FILING DATE: 2004-03-16  
PRIOR APPLICATION NUMBER: US 09/956,425  
PRIOR FILING DATE: 2001-09-19  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 491  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-489-802-8  
Query Match 99.3%; Score 550; DB 17; Length 491;

Best Local Similarity 99.1%; Pred. No. 1.4e-56;  
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SQIPASQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVY 60  
DB 17 SQIPASQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVY 76  
QY 61 CSNDLLGDLFGVPFSVKHRKIYTMIRNLVVNQESSDSGTSVSEN 109  
DB 77 CSNDLLGDLFGVPFSVKHRKIYTMIRNLVVNQESSDSGTSVSEN 125  
RESULT 10  
US-10-723-860-2236  
Sequence 2236, Application US/10723860  
Publication No. US20040253606A1  
GENERAL INFORMATION:  
APPLICANT: Aziz, Nataasha  
APPLICANT: Ginsburg, Wendy M.  
APPLICANT: Zlotnik, Albert  
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &  
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators  
FILE REFERENCE: 05882.0193.NPUS01  
CURRENT APPLICATION NUMBER: US/10/723,860  
CURRENT FILING DATE: 2003-11-26  
PRIOR APPLICATION NUMBER: 60/429,739  
PRIOR FILING DATE: 2002-11-26  
NUMBER OF SEQ ID NOS: 8393  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 2236  
LENGTH: 491  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-723-860-2236

Query Match 99.3%; Score 550; DB 17; Length 491;  
Best Local Similarity 99.1%; Pred. No. 1.4e-56;  
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SQIPASQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVY 60  
DB 17 SQIPASQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVY 76  
QY 61 CSNDLLGDLFGVPFSVKHRKIYTMIRNLVVNQESSDSGTSVSEN 109  
DB 77 CSNDLLGDLFGVPFSVKHRKIYTMIRNLVVNQESSDSGTSVSEN 125

RESULT 11  
US-10-057-510-4  
Sequence 4, Application US/10057510  
Publication No. US20020098580A1  
GENERAL INFORMATION:  
APPLICANT: Nandabalan, Krishnan  
APPLICANT: Yang, Meijia  
APPLICANT: Schulz, Vincent  
APPLICANT: Curagen Corporation  
TITLE OF INVENTION: MDM INTERACTING PROTEIN AND METHODS OF USE THEREOF  
FILE REFERENCE: 15966-524 MDM US  
CURRENT APPLICATION NUMBER: US/10/057,510  
CURRENT FILING DATE: 2002-01-25  
PRIOR APPLICATION NUMBER: USN 09/510,252  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: USN 60/121,192  
PRIOR FILING DATE: 1999-02-23  
PRIOR APPLICATION NUMBER: USN 60/122,643  
PRIOR FILING DATE: 1999-03-03  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4  
LENGTH: 216  
TYPE: PRT  
ORGANISM: Homo sapiens

US-10-057-510-4

Query Match 96.3%; Score 533.5; DB 13; Length 216;  
Best Local Similarity 98.2%; Pred. No. 4.4e-55;  
Matches 107; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 SQIPASEQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLYLQYIMTKRLYDEKQOHIVY 60  
|||||  
Db 17 SQIPASEQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLYL-QYIMTKRLYDEKQOHIVY 75  
|||||  
QY 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIVRNLVVNVNQESSDSGTSVSEN 109  
|||||  
Db 76 CSNDLLGDLFGVPSFSVKEHRKIYTMIVRNLVVNVNQESSDSGTSVSEN 124  
|||||

## RESULT 12

US-10-287-226-380  
; Sequence 380, Application US/10287226  
; Publication No. US20040086875A1

; GENERAL INFORMATION:  
; APPLICANT: Agee, Michele L.,

; APPLICANT: Alsobrook, John P.,  
; APPLICANT: Berghs, Constance,

; APPLICANT: Boldog, Ference,

; APPLICANT: Burgess, Catherine E.,

; APPLICANT: Chant, John S.,

; APPLICANT: Chaudhuri, Amitabha,

; APPLICANT: DiPippo, Vincent A.,

; APPLICANT: Edinger, Shlomit R.,

; APPLICANT: Eisen, Andrew,

; APPLICANT: Ellerman, Karen,

; APPLICANT: Gangolli, Esha A.,

; APPLICANT: Gorman, Linda,

; APPLICANT: Gerlach, Valerie,

; APPLICANT: Ji, Weizhen,

; APPLICANT: Kekuda, Ramesh,

; APPLICANT: Khramtsov, Nikolai,

; APPLICANT: Li, Li,

; APPLICANT: Malyankar, Uriel M.,

; APPLICANT: MacDougall, John R.,

; APPLICANT: Mezes, Peter S.,

; APPLICANT: Miller, Charles E.,

; APPLICANT: Millet, Isabelle,

; APPLICANT: Ooi, Chean Eng,

; APPLICANT: Padigaru, Muralidhara,

; APPLICANT: Patturajan, Meera,

; APPLICANT: Rastelli, Luca,

; APPLICANT: Rieger, Daniel K.,

; APPLICANT: Rothenberg, Mark E.,

; APPLICANT: Shenoy, Suresh G.,

; APPLICANT: Spaderna, Steven K.,

; APPLICANT: Spytek, Kimberley A.,

; APPLICANT: Taupier, Jr., Raymond J.,

; APPLICANT: Vernet, Corine A.M.,

; APPLICANT: Zethusen, Bryan D.,

; APPLICANT: Zhong, Mei

; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

; FILE REFERENCE: 21402-480C

; CURRENT APPLICATION NUMBER: US/10/287,226

; CURRENT FILING DATE: 2002-11-04

; PRIOR APPLICATION NUMBER: 60/334,421

; PRIOR FILING DATE: 2001-11-30

; PRIOR APPLICATION NUMBER: 60/354,392

; PRIOR FILING DATE: 2002-02-04

; PRIOR APPLICATION NUMBER: 60/360,148

; PRIOR FILING DATE: 2002-02-27

; PRIOR APPLICATION NUMBER: 60/364,000

; PRIOR FILING DATE: 2002-03-13

; PRIOR APPLICATION NUMBER: 60/404,821

; PRIOR FILING DATE: 2002-08-20

; PRIOR APPLICATION NUMBER: 60/334,526

; PRIOR FILING DATE: 2001-11-30

; PRIOR APPLICATION NUMBER: 60/354,409  
; PRIOR FILING DATE: 2002-02-04  
; PRIOR APPLICATION NUMBER: 60/364,227  
; PRIOR FILING DATE: 2002-03-13  
; PRIOR APPLICATION NUMBER: 60/334,027  
; PRIOR FILING DATE: 2001-11-28  
; PRIOR APPLICATION NUMBER: 60/331,641  
; PRIOR FILING DATE: 2001-11-20  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 673  
; SOFTWARE: CuraSeqList version 0.1  
; SEQ ID NO 380  
; LENGTH: 522  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-287-226-380

Query Match 94.7%; Score 524.5; DB 15; Length 522;

Best Local Similarity 77.1%; Pred. No. 1.7e-53;  
Matches 108; Conservative 1; Mismatches 0; Indels 31; Gaps 1;

QY 1 SQIPASEQETLVPRKPLLLKLLKSVGAQKDTYTMKE----- 36

Db 17 SQIPASEQETLVPRKPLLLKLLKSVGAQKDTYTMKEWSFTMLPRLVNSWAQGLPRP 76

QY 37 -----VLYLQYIMTKRLYDEKQOHIVYCSNDLLGDLFGVPSFSVKEHRKIYTMIVR 89

Db 77 PKVLDLQVLYLQYIMTKRLYDEKQOHIVYCSNDLLGDLFGVPSFSVKEHRKIYTMIVR 136

QY 90 NLVVNVNQESSDSGTSVSEN 109

Db 137 NLVVNVNQESSDSGTSVSEN 156

## RESULT 13

US-10-287-226-382

; Sequence 382, Application US/10287226

; Publication No. US20040086875A1

; GENERAL INFORMATION:

; APPLICANT: Agee, Michele L.,

; APPLICANT: Alsobrook, John P.,

; APPLICANT: Berghs, Constance,

; APPLICANT: Boldog, Ference,

; APPLICANT: Burgess, Catherine E.,

; APPLICANT: Chant, John S.,

; APPLICANT: Chaudhuri, Amitabha,

; APPLICANT: DiPippo, Vincent A.,

; APPLICANT: Edinger, Shlomit R.,

; APPLICANT: Eisen, Andrew,

; APPLICANT: Ellerman, Karen,

; APPLICANT: Gangolli, Esha A.,

; APPLICANT: Gorman, Linda,

; APPLICANT: Gerlach, Valerie,

; APPLICANT: Ji, Weizhen,

; APPLICANT: Kekuda, Ramesh,

; APPLICANT: Khramtsov, Nikolai,

; APPLICANT: Li, Li,

; APPLICANT: Malyankar, Uriel M.,

; APPLICANT: MacDougall, John R.,

; APPLICANT: Mezes, Peter S.,

; APPLICANT: Millet, Charles E.,

; APPLICANT: Millet, Isabelle,

; APPLICANT: Ooi, Chean Eng,

; APPLICANT: Ort, Tatiana,

; APPLICANT: Padigaru, Muralidhara,

; APPLICANT: Patturajan, Meera,

; APPLICANT: Rastelli, Luca,

; APPLICANT: Rieger, Daniel K.,

; APPLICANT: Rothenberg, Mark E.,

; APPLICANT: Shenoy, Suresh G.,

; APPLICANT: Spaderna, Steven K.,

; APPLICANT: Spytek, Kimberley A.,

; APPLICANT: Taupier, Jr., Raymond J.,

; APPLICANT: Vernet, Corine A.M.,

; APPLICANT: Zethusen, Bryan D.,

; APPLICANT: Zhong, Mei

; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

; FILE REFERENCE: 21402-480C

; CURRENT APPLICATION NUMBER: US/10/287,226

; CURRENT FILING DATE: 2002-11-04

; PRIOR APPLICATION NUMBER: 60/334,421

; PRIOR FILING DATE: 2001-11-30

; PRIOR APPLICATION NUMBER: 60/354,392

; PRIOR FILING DATE: 2002-02-04

; PRIOR APPLICATION NUMBER: 60/360,148

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; APPLICANT: Vernet, Corine A.M.,
; APPLICANT: Zehrusen, Bryan D.,
; APPLICANT: Zhong, Mel
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-480C
; CURRENT APPLICATION NUMBER: US/10/287,226
; CURRENT FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: 60/334,421
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/354,392
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/360,148
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: 60/364,000
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/404,821
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 60/334,526
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/354,409
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/364,227
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/334,027
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/331,641
; PRIOR FILING DATE: 2001-11-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 673
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 382
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-226-382

Query Match 94.7%; Score 524.5; DB 15; Length 522;
Best Local Similarity 77.1%; Pred. No. 1.7e-53;
Matches 108; Conservative 1; Mismatches 0; Indels 31; Gaps 1;

QY 1 SQIPASEQETLVPRKPLLLKLLKSVGAQKDTYTMKE----- 36
DB 17 SQIPASEQETLVPRKPLLLKLLKSVGAQKDTYTMKEKRSFTMLPLVLVNSNAQGICLPRP 76
QY 37 -----VLVYLGOYIMTKRLYDEKQOHIYVCSNDLLGDLFGVPSFVKHKRIYTMIVR 89
DB 77 PKVLQLQVLFYIGQYIMTKRLYDEKQOHIYVCSNDLLGDLFGVPSFVKHKRIYTMIVR 136
QY 90 NLVWVNOQSSDSGTSVSEN 109
DB 137 NLVWVNOQSSDSGTSVSEN 156

RESULT 14
US-09-956-425-6
; Sequence 6, Application US/09956425
; Patent No. US20020045192A1
; GENERAL INFORMATION:
; APPLICANT: Kriwacki, Richard
; APPLICANT: Bothner, Brian
; APPLICANT: Lewis, William
; TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and Method of Use Thereof
; CURRENT APPLICATION NUMBER: US/09/956,425
; CURRENT FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-956-425-6
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Query Match 88.5%; Score 490.5; DB 9; Length 489;
Best Local Similarity 87.2%; Pred. No. 1.7e-49;
Matches 95; Conservative 8; Mismatches 3; Indels 3; Gaps 1;

QY 1 SQIPASEQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLVYLGOYIMTKRLYDEKQOHIYV 60
DB 17 SQIPASEQETLVPRKPLLLKLLKSVGAQNDITYTMKEIIFYIGQYIMTKRLYDEKQOHIYV 76
QY 61 CSNDLLGDLFGVPSFVKHKRIYTMIVRNLVVWVNOQSSDSGTSVSEN 109
DB 77 CSNDLLGDLFGVPSFVKHKRIYAMIVRNLVAVSQQ---DSGTSLSSES 122

RESULT 15
US-09-966-724-4
; Sequence 4, Application US/09966724
; Publication No. US20040170971A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; HUMAN TUMORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G ST., N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/966,724
; FILING DATE: 01-Oct-2001
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/044,619
; FILING DATE: 2001-10-01
; APPLICATION NUMBER: US 07/867,840
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.40148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-966-724-4

Query Match 88.5%; Score 490.5; DB 11; Length 489;
Best Local Similarity 87.2%; Pred. No. 1.7e-49;
Matches 95; Conservative 8; Mismatches 3; Indels 3; Gaps 1;

QY 1 SQIPASEQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLVYLGOYIMTKRLYDEKQOHIYV 60
DB 17 SQIPASEQETLVPRKPLLLKLLKSVGAQNDITYTMKEIIFYIGQYIMTKRLYDEKQOHIYV 76
QY 61 CSNDLLGDLFGVPSFVKHKRIYTMIVRNLVVWVNOQSSDSGTSVSEN 109
DB 77 CSNDLLGDLFGVPSFVKHKRIYAMIVRNLVAVSQQ---DSGTSLSSES 122
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

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(without alignments)  
325.615 Million cell updates/sec

Title: US-10-822-254-8  
Perfect score: 554  
Sequence: 1 SOIPASEQETLVPRPKPLLLK.....NLVVNQESSDSGTSVSEN 109

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/1aa/5B COMB.pap:\*  
3: /cgn2\_6/ptodata/1/1aa/6A COMB.pap:\*  
4: /cgn2\_6/ptodata/1/1aa/6B COMB.pap:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS COMB.pap:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	550	99.3	188	4	US-09-603-052-4
2	550	99.3	491	1	US-07-903-103-2
3	550	99.3	491	1	US-08-044-619A-2
4	550	99.3	491	1	US-08-283-911-2
5	550	99.3	491	1	US-08-245-500A-3
6	550	99.3	491	1	US-08-390-546-3
7	550	99.3	491	1	US-08-390-479A-3
8	550	99.3	491	1	US-08-557-393-3
9	550	99.3	491	1	US-08-390-516C-3
10	550	99.3	491	1	US-08-390-517A-3
11	550	99.3	491	1	US-08-390-515A-3
12	550	99.3	491	2	US-08-801-718-3
13	550	99.3	491	3	US-09-170-159A-3
14	550	99.3	491	4	US-09-480-718-4
15	533.5	96.3	216	3	US-09-510-252-4
16	490.5	88.5	489	1	US-07-903-103-4
17	490.5	88.5	489	1	US-08-044-619A-4
18	490.5	88.5	489	1	US-08-283-911-4
19	490.5	88.5	489	1	US-08-245-500A-5
20	490.5	88.5	489	1	US-08-390-546-5
21	490.5	88.5	489	1	US-08-390-479A-5
22	490.5	88.5	489	1	US-08-557-393-5
23	490.5	88.5	489	1	US-08-390-516C-5
24	490.5	88.5	489	1	US-08-390-517A-5
25	490.5	88.5	489	1	US-08-390-515A-5
26	490.5	88.5	489	2	US-08-801-718-5
27	490.5	88.5	489	3	US-09-170-159A-5

28	490.5	88.5	489	4	US-09-480-718-46	Sequence 46, Appl
29	176	31.8	243	4	US-09-786-702-2	Sequence 2, Appl
30	72.5	13.1	244	4	US-09-543-681A-6675	Sequence 6675, Ap
31	70.5	12.7	420	4	US-09-270-767-43304	Sequence 43304, A
32	67	12.1	62	4	US-09-248-766A-24446	Sequence 24446, A
33	66.5	12.0	104	4	US-09-270-767-41801	Sequence 41801, A
34	66.5	12.0	590	3	US-09-232-191-25	Sequence 25, Appl
35	66.5	12.0	590	3	US-09-232-200-75	Sequence 75, Appl
36	66.5	12.0	590	3	US-09-232-197-75	Sequence 75, Appl
37	66.5	12.0	590	3	US-09-232-201-75	Sequence 75, Appl
38	66.5	12.0	590	4	US-09-232-195-75	Sequence 75, Appl
39	65.5	11.8	445	4	US-09-583-110-414	Sequence 414, Ap
40	65	11.7	2938	5	PCT-US94-00198-3	Sequence 3, Appl
41	64.5	11.6	107	3	US-09-187-859-35	Sequence 35, Appl
42	64.5	11.6	107	3	US-09-187-859-36	Sequence 36, Appl
43	64.5	11.6	107	4	US-09-839-542B-35	Sequence 35, Appl
44	64.5	11.6	107	4	US-09-839-542B-36	Sequence 36, Appl
45	64.5	11.6	107	4	US-09-535-852-35	Sequence 35, Appl

## ALIGNMENTS

### RESULT 1

US-09-603-052-4  
; Sequence 4, Application US/09603052  
; Patent No. 6492116  
; GENERAL INFORMATION:  
; APPLICANT: Chene, Patrick  
; APPLICANT: Hochkeppel, Heinz-Kurt  
; TITLE OF INVENTION: Assay for identifying inhibitors of the interaction  
; FILE REFERENCE: MEWB26.001C1  
; CURRENT APPLICATION NUMBER: US/09/603,052  
; CURRENT FILING DATE: 2000-06-26  
; PRIOR APPLICATION NUMBER: EP 95810576.9  
; PRIOR FILING DATE: 1995-09-18  
; PRIOR APPLICATION NUMBER: PCT/EP96/03957  
; PRIOR FILING DATE: 1996-09-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 188  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-603-052-4

Query Match 99.3%; Score 550; DB 4; Length 188;  
Best Local Similarity 99.1%; Pred. No. 4.7e-61;  
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SOIPASEQETLVPRPKPLLLKLSVGAOKDTYTKKEVLVYLGQYIMTKRLVDEKQOHIVY 60  
Db 17 SOIPASEQETLVPRPKPLLLKLSVGAOKDTYTKKEVLVYLGQYIMTKRLVDEKQOHIVY 76  
Qy 61 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 109  
Db 77 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 125

### RESULT 2

US-07-903-103-2  
; Sequence 2, Application US/07903103  
; Patent No. 5411860  
; GENERAL INFORMATION:  
; APPLICANT: VOGELSTEIN, BERT  
; APPLICANT: KINZLER, KENNETH  
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
; STREET: 1001 G ST., N.W.

;; CITY: WASHINGTON  
;; STATE: D.C.  
;; COUNTRY: USA  
;; ZIP: 20001-4597  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/07/903,103  
;; FILING DATE: 19920623  
;; CLASSIFICATION: 435  
;;  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/867,840  
;; FILING DATE: 07-APR-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: KAGAN, SARAH A.  
;; REGISTRATION NUMBER: 32,141  
;; REFERENCE/DOCKET NUMBER: 01107.40148  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-508-9100  
;; TELEFAX: 202-508-9299  
;;  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 491 amino acids  
;; TYPE: AMINO ACID  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;;  
US-07-903-103-2

Query Match 99.3%; Score 550; DB 1; Length 491;  
Best Local Similarity 99.1%; Pred. No. 1.7e-60;  
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVY 60  
DB 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVY 76  
  
QY 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 109  
DB 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 125

RESULT 3  
US-08-044-619A-2  
; Sequence 2, Application US/08044619A  
; Patent No. 5420263  
; GENERAL INFORMATION:  
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY  
; APPLICANT: 720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA  
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
; TITLE OF INVENTION: HUMAN TUMORS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
; STREET: 1001 G ST., N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20001-4597  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/044,619A  
; FILING DATE: 07-APR-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/903,103

;; FILING DATE: 23-JUN-1992  
;; APPLICATION NUMBER: US 07/867,840  
;; FILING DATE: 07-APR-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: KAGAN, SARAH A.  
;; REGISTRATION NUMBER: 32,141  
;; REFERENCE/DOCKET NUMBER: 01107.40148  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-508-9100  
;; TELEFAX: 202-508-9299  
;;  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 491 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;;  
US-08-044-619A-2

Query Match 99.3%; Score 550; DB 1; Length 491;  
Best Local Similarity 99.1%; Pred. No. 1.7e-60;  
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVY 60  
DB 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVY 76  
  
QY 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 109  
DB 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 125

RESULT 4  
US-08-283-911-2  
; Sequence 2, Application US/08283911  
; Patent No. 5519118  
; GENERAL INFORMATION:  
; APPLICANT: VOGELSTEIN, BERT  
; APPLICANT: KINZLER, KENNETH  
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
; TITLE OF INVENTION: HUMAN TUMORS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
; STREET: 1001 G ST., N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20001-4597  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/283,911  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/903,103  
; FILING DATE: 23-JUN-1992  
; APPLICATION NUMBER: US 07/867,840  
; FILING DATE: 07-APR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KAGAN, SARAH A.  
; REGISTRATION NUMBER: 32,141  
; REFERENCE/DOCKET NUMBER: 01107.40148  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-508-9100  
; TELEFAX: 202-508-9299  
; TELETYPE: 197430 BBMB UT  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:

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/ ; LENGTH: 491 amino acids
/ ; TYPE: amino acid
/ ; TOPOLOGY: linear
/ ; MOLECULE TYPE: protein
US-08-283-911-2

Query Match          99.3%; Score 550; DB 1; Length 491;
Best Local Similarity 99.1%; Pred. No. 1.7e-60;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLYLGYIMTKRLYDEKQOHIVY 60
Db 17 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLYLGYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPSPSVKEHRKIYTMIRNLVVNQSSSDSGTSVSEN 109
Db 77 CSNDLLGDLFGVPSPSVKEHRKIYTMIRNLVVNQSSSDSGTSVSEN 125

RESULT 5
US-08-245-500A-3
; Sequence 3, Application US/08245500A
; Patent No. 5550023
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/245.500A
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BMB UT
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-245-500A-3

Query Match          99.3%; Score 550; DB 1; Length 491;
Best Local Similarity 99.1%; Pred. No. 1.7e-60;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLYLGYIMTKRLYDEKQOHIVY 60
Db 17 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLYLGYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPSPSVKEHRKIYTMIRNLVVNQSSSDSGTSVSEN 109
Db 77 CSNDLLGDLFGVPSPSVKEHRKIYTMIRNLVVNQSSSDSGTSVSEN 125

US-08-390-546-3
; Sequence 3, Application US/08390546
; Patent No. 5606044
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390.546
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BMB UT
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-390-546-3

Query Match          99.3%; Score 550; DB 1; Length 491;
Best Local Similarity 99.1%; Pred. No. 1.7e-60;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLYLGYIMTKRLYDEKQOHIVY 60
Db 17 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLYLGYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPSPSVKEHRKIYTMIRNLVVNQSSSDSGTSVSEN 109
Db 77 CSNDLLGDLFGVPSPSVKEHRKIYTMIRNLVVNQSSSDSGTSVSEN 125

US-08-479A-3
; Sequence 3, Application US/08390479A
; Patent No. 5618921
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
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; ADDRESSEE: BANNER & WITCOFF, LTD.
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,479A
; FILING DATE: 02-FEB-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.48992
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-390-479A-3
;
; Query Match 99.3%; Score 550; DB 1; Length 491;
; Best Local Similarity 99.1%; Pred. No. 1.7e-60;
; Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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; DB 17 SQIPASEQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLYLGOYIMTKRLYDEKQOHIVY 76
; |
; QY 61 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVNQESSDSGTSVSEN 109
; |
; DB 77 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVNQESSDSGTSVSEN 125
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;
; RESULT 8
; US-08-557-393-3
; Sequence 3, Application US/08557393
; Patent No. 5702903
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,393
; FILING DATE: 13-NOV-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;
; ADDRESSSEE: BANNER & WITCOFF, LTD.
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,479A
; FILING DATE: 02-FEB-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.48992
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-390-479A-3
;
; Query Match 99.3%; Score 550; DB 1; Length 491;
; Best Local Similarity 99.1%; Pred. No. 1.7e-60;
; Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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; QY 1 SQIPASEQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLYLGOYIMTKRLYDEKQOHIVY 60
; |
; DB 17 SQIPASEQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLYLGOYIMTKRLYDEKQOHIVY 76
; |
; QY 61 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVNQESSDSGTSVSEN 109
; |
; DB 77 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVNQESSDSGTSVSEN 125
; |
;
; RESULT 9
; US-08-390-516C-3
; Sequence 3, Application US/08390516C
; Patent No. 5708136
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,516C
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-557-393-3
;
; Query Match 99.3%; Score 550; DB 1; Length 491;
; Best Local Similarity 99.1%; Pred. No. 1.7e-60;
; Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 SQIPASEQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLYLGOYIMTKRLYDEKQOHIVY 60
; |
; DB 17 SQIPASEQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLYLGOYIMTKRLYDEKQOHIVY 76
; |
; QY 61 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVNQESSDSGTSVSEN 109
; |
; DB 77 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVNQESSDSGTSVSEN 125
; |
;
; RESULT 9
; US-08-390-516C-3
; Sequence 3, Application US/08390516C
; Patent No. 5708136
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,516C
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-557-393-3
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US-08-390-516C-3

Query Match	99.3%;	Score 550;	DB 1;	Length 491;
Best Local Similarity	99.1%;	Pred. No. 1.7e-60;		
Matches 108;	Conservative	1;	Mismatches 0;	Indels 0;
			Gaps 0;	
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<i>b</i>	17	SOIPASEQETLYRPPKPLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTRLYDEKQOHIVY	76	
<i>y</i>	61	CSNDLLGLDLFGVPSPSVKEHKIYTMIVRNLYVNNQOESSDSGTSVSN	109	
	77	CSNDLLGLDLFGVPSPSVKEHKIYTMIVRNLYVNNQOESSDSGTSVSN	125	

## RESULT 10

US-08-390-517A-3  
; Sequence 3, Application US/08390517A  
; Patent No. 5736338  
; GENERAL INFORMATION:  
; APPLICANT: BURRELL, MARILEE  
; APPLICANT: HILL, DAVID E.  
; APPLICANT: KINZLER, KENNETH W.  
; APPLICANT: VOGELSTEIN, BERT  
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
; TITLE OF INVENTION: HUMAN TUMORS  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
; STREET: 1001 G STREET, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/390,517A  
; FILING DATE: 07-APR-1993

	Query Match	99.3%	Score 550;	DB 1;	Length 491;
	Best Local Similarity	99.1%	Pred. No. 1.7e-60;		
	Matches 108;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	SQIPASEQETLVRPKPLLLKLLKLSVGAQKDTYMKVEVLYYLGVYIMTKRLYDEKQHHVY	60		
Db	17	SQIPASEQETLVRPKPLLLKLLKLSVGAQKDTYMKVEVLYYLGVYIMTKRLYDEKQHHVY	76		
QY	61	CSNDLLGDLFGVPSFSVKEHRKIYTIMYRNLLVVNNQOESSDSGTSVSEN	109		
Db	77	CSNDLLGDLFGVPSFSVKEHRKIYTIMYRNLLVVNNQOESSDSGTSVSEN	125		

## RESULT 11

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US-08-390-515A-3
; Sequence 3, Application US/08390515A
; Patent No. 5756455
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/390,515A
; APPLICATION NUMBER: 07-APR-1993
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BMB UT
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-390-515A-3

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	Query Match	99.3%	Score 550;	DB 1;	Length 491;
	Best Local Similarity	99.1%;	Pred. No. 1.7e-60;		
	Matches 108;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	SQIPASEQETLVRPKPELLKLLKSVGAQKDTYTMKEVLYYLGYIMTKRLYDEKQHHIVY	60		
Db	17	SQIPASEQETLVRPKPELLKLLKSVGAQKDTYTMKEVLYYLGYIMTKRLYDEKQHHIVY	76		
Qy	61	CSNDLLGDLFGVPSPFSVKEHRKIYTIMYRNLLVVNQOESSDSTGSYSEN	109		
Db	77	CSNDLLGDLFGVPSPFSVKEHRKIYTIMYRNLLVVNQOESSDSTGSYSEN	125		

## RESULT 12

US-08-801-718-3  
; Sequence 3, Application US/08801718  
; Patent No. 5858976  
; GENERAL INFORMATION:  
; APPLICANT: BURRELL, MARILEE  
; APPLICANT: HILL, DAVID E.  
; APPLICANT: KINZLER, KENNETH W.  
; APPLICANT: VOGELSTEIN, BERT  
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
; TITLE OF INVENTION: HUMAN TUMORS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
; STREET: 1001 G STREET, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.

us-10-822-254-8.ra1

Fri Jan 28 09:36:26 2005

```

; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,718
; FILING DATE: 14-FEB-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/390,515
; FILING DATE: 07-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-801-718-3

Query Match 99.3%; Score 550; DB 2; Length 491;
Best Local Similarity 99.1%; Pred. No. 1.7e-60;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVY 60
Db 17 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVY 76
QY 61 CSNDLLGDLFGVPFSVKHKKIYTMIRNVLVNVNQESSDSGTSVSEN 109
Db 77 CSNDLLGDLFGVPFSVKHKKIYTMIRNVLVNVNQESSDSGTSVSEN 125

RESULT 14
US-09-480-718-44
; Sequence 44, Application US/09480718
; Patent No. 6407062
; GENERAL INFORMATION:
; APPLICANT: Sherr, Charles J
; APPLICANT: Quelle, Dawn E
; APPLICANT: Weber, Jason D.
; APPLICANT: Rousset, Martine F.
; APPLICANT: Frederique, Zindy
; TITLE OF INVENTION: ARF-19, A NOVEL REGULATOR OF THE MAMMALIAN CELL CYCLE
; FILE REFERENCE: 1340-1-023 CIP 1
; CURRENT APPLICATION NUMBER: US/09/480,718
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 09/129,855
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 44
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-480-718-44

Query Match 99.3%; Score 550; DB 4; Length 491;
Best Local Similarity 99.1%; Pred. No. 1.7e-60;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVY 60
Db 17 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVY 76
QY 61 CSNDLLGDLFGVPFSVKHKKIYTMIRNVLVNVNQESSDSGTSVSEN 109
Db 77 CSNDLLGDLFGVPFSVKHKKIYTMIRNVLVNVNQESSDSGTSVSEN 125

RESULT 15
US-09-510-252-4
; Sequence 4, Application US/09510252
; Patent No. 6372490
; GENERAL INFORMATION:
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Yang, Meijia
; APPLICANT: Schulz, Vincent

```



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; APPLICANT: CuraGen Corporation
; TITLE OF INVENTION: MDM INTERACTING PROTEIN AND METHODS OF USE THEREOF
; FILE REFERENCE: 15966-524 MDM US
; CURRENT APPLICATION NUMBER: US/09/510,252
; CURRENT FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: USSN 60/121,192
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: USSN 60/122,643
; PRIOR FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-510-252-4

Query Match      96.3%; Score 533.5; DB 3; Length 216;
Best Local Similarity 98.2%; Pred. No. 6.7e-59;
Matches 107; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY      1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLQYIMTKRLYDEKQOHIVY 60
        |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVYL-QYIMTKRLYDEKQOHIVY 75

QY      61 CSNDLLGDLFGVPSPSVKEHRKIYTMIVRNLVVNNQESSDSGTSVSEN 109
        |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      76 CSNDLLGDLFGVPSPSVKEHRKIYTMIVRNLVVNNQESSDSGTSVSEN 124

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Search completed: January 27, 2005, 18:17:07  
Job time : 23.2 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:51:46 ; Search time 84.6 Seconds  
(without alignments)  
741.322 Million cell updates/sec

Title: US-10-822-254-8

Perfect score: 554

Sequence: 1 SQIPASQETLVRPKPLLLK.....NLVVNQESSDSGTSVSEN 109

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	550	99.3	166	Q8NDW2	Q8ndw2 homo sapien
2	550	99.3	195	Q96DS4	Q96ds4 homo sapien
3	550	99.3	243	Q8TE47	Q8te47 homo sapien
4	550	99.3	491	1 MDM2 HUMAN	Q00987 homo sapien
5	550	99.3	491	2 AAP35922	Aap35922 homo sapi
6	550	99.3	491	2 AAH67077	Aah67077 homo sapi
7	538	97.1	487	1 MDM2 CANFA	P56950 canis famil
8	538	97.1	487	2 Q9GMZ6	Q9gmz6 canis famil
9	538	97.1	491	1 MDM2 HORSE	P56951 equus cabal
10	535	96.6	491	2 Q7YRZ8	Q7yrz8 felis silve
11	500	90.3	436	2 Q8WYJ2	Q8wyj2 homo sapien
12	490.5	88.5	489	1 MDM2 MOUSE	P23804 mus musculu
13	490.5	88.5	489	2 Q9LXK7	Q9lxx7 m mus muscu
14	473	85.4	118	2 Q8WYJ3	Q8wyj3 homo sapien
15	468.5	84.6	466	1 MDM2 MESAU	Q60524 mesocricetu
16	412	74.4	325	2 Q9PVL2	Q9pvl2 gallus gall
17	404	72.9	173	2 Q8TE46	Q8te46 homo sapien
18	362	65.3	473	1 MDM2 XENLA	P56273 xenopus lae
19	362	65.3	473	2 Q6GMB5	Q6gmb5 xenopus lae
20	361	65.2	482	2 Q6P3Q9	Q6p3q9 xenopus tro
21	361	65.2	482	2 AAH63898	Aah63898 xenopus t
22	336	60.6	105	2 Q8NDW0	Q8ndw0 homo sapien
23	320	57.8	426	2 Q9GK41	Q9gk41 canis famil
24	289.5	52.3	445	1 MDM2 BRARE	O42354 brachydanio
25	289.5	52.3	445	2 AA00198	Aam00198 brachydan
26	280.5	50.6	446	2 Q8WYJ1	Q8wyj1 homo sapien
27	279.5	50.5	489	1 MDM4 MOUSE	O35618 mus musculu
28	276.5	49.9	489	2 Q8CYG1	Q8cyg1 m mus muscu
29	271	48.9	491	2 Q7ZUW7	Q7zuw7 brachydanio
30	270	48.7	490	2 Q99L86	Q99l86 mus musculu
31	269	48.6	475	2 Q7ZYI3	Q7zyi3 xenopus lae

32	257.5	46.5	134	2 Q6PHL8	Q6phl8 xenopus lae
33	257.5	46.5	134	2 AAH56503	Aah56503 xenopus l
34	254	45.8	153	2 Q6MZR7	Q6mzr7 homo sapien
35	254	45.8	153	2 CAE45961	Ca45961 homo sapi
36	254	45.8	490	2 AAH67299	Aah67299 homo sapi
37	252	45.5	490	1 MDM4 HUMAN	O15151 homo sapien
38	220	39.7	69	2 Q86WA4	Q86wa4 homo sapien
39	213	38.4	66	2 Q96DS3	Q96ds3 homo sapien
40	210	37.9	70	2 Q86WA3	Q86wa3 homo sapien
41	196	35.4	95	2 Q96DS1	Q96ds1 homo sapien
42	179.5	32.4	70	2 Q8NDW1	Q8ndw1 homo sapien
43	177	31.9	159	2 Q96DS0	Q96ds0 homo sapien
44	176	31.8	60	2 Q96DS5	Q96ds5 homo sapien
45	176	31.8	130	2 Q9H4C3	Q9h4c3 homo sapien

#### ALIGNMENTS

##### RESULT 1

ID	Q8NDW2	PRELIMINARY;	PRT;	166 AA.
AC	Q8NDW2;			
DT	01-OCT-2002 (TrEMBLrel. 22, Created)			
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)			
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)			
DE	P53-binding protein.			
GN	Name=MDM2;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Bartel F., Pinkert D., Kappler M., Rache M., Schmidt H., Taubert H.;			
RL	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AJ491698; CAD36959.1; -.			
DR	HSSP; Q9UNT8; 1YCR.			
DR	GO; GO:0005634; C:nucleus; IEA.			
DR	InterPro; IPR010984; MDM2.			
DR	InterPro; IPR003121; SWIB_MDM2.			
DR	Pfam; PF02201; SWIB; 1.			
SQ	SEQUENCE 166 AA; 18900 MW; FA6BSBA18E85040D CRC64;			

Query Match 99.3%; Score 550; DB 2; Length 166;  
Best Local Similarity 99.1%; Pred. No. 8.8e-51;  
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASQETLVRPKPLLLKLSVGAKQDTYTKVELVYLGQYIMTKRLYDEKQOHIVY 60

Db 17 SQIPASQETLVRPKPLLLKLSVGAKQDTYTKVELVYLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLGVPSPFSVKEHKIYTMTRYNLVVNQESSDSGTSVSEN 109

Db 77 CSNDLLGDLGVPSPFSVKEHKIYTMTRYNLVVNQESSDSGTSVSEN 125

##### RESULT 2

ID	Q96DS4	PRELIMINARY;	PRT;	195 AA.
AC	Q96DS4;			
DT	01-DEC-2001 (TrEMBLrel. 19, Created)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)			
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)			
DE	MDM2 variant FB26.			
GN	Name=MDM2;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Rhabdomyosarcoma tumor;			

RA Bartel F., Taylor A.C., Taubert H., Harris L.C.;  
 RL Submitted (MAY-2001) to the ENBL/GenBank/DBJ databases.

DR EMBL; AF385323; AAL13243.1; -;  
 DR HSSP; Q9UMT8; 1YCR.

DR GO; GO:0005634; C:nucleus; IEA.

DR InterPro; IPR010984; MDM2.

DR InterPro; IPR003121; SWIB\_MDM2.

DR Pfam; PF02201; SWIB; 1.

SQ SEQUENCE 195 AA; 22161 MW; 4987AE567DB12D5D CRC64;

Query Match 99.3%; Score 550; DB 2; Length 195;  
 Best Local Similarity 99.1%; Pred. No. 1.1e-50;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASQETLVRRPKPLLLKLLKSVGAQKDTYTMKEVLYLGGYIMTKRLYDEKQOHIVY 60

Db 17 SQIPASEQETLVRRPKPLLLKLLKSVGAQKDTYTMKEVLYLGGYIMTKRLYDEKQOHIVY 76

Qy 61 CSNLLGLDGLFGVPSFVKHRRKIYTMIRNLVNVNQESSDGSSTSVSEN 109

Db 77 CSNLLGLDGLFGVPSFVKHRRKIYTMIRNLVNVNQESSDGSSTSVSEN 125

# RESULT 3

Q8TE47 PRELIMINARY; PRT; 243 AA.

ID Q8TE47

AC Q8TE47

DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE MDM2 isoform KB9 protein.

GN Name=MDM2 isoform KB9;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN (1)

RP SEQUENCE FROM N.A. (ISOFORM MDM2).

RC TISSUE=Lymphocytes;

RA Bartel F., Pinkert D., Kappler M., Bache M., Schmidt H., Taubert H.;

RL Submitted (FEB-2002) to the ENBL/GenBank/DBJ databases.

DR EMBL; AJ430612; CAD23251.1; -;

DR HSSP; Q9UMT8; 1YCR.

DR GO; GO:0005634; C:nucleus; IEA.

DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.

DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.

DR GO; GO:0016567; P:protein ubiquitination; IEA.

DR InterPro; IPR010984; MDM2.

DR InterPro; IPR003121; SWIB\_MDM2.

DR Pfam; PF02201; SWIB; 1.

DR SMART; SM00184; RING; 1.

DR PROSITE; PS0089; ZF\_RING\_2; 1.

SQ SEQUENCE 243 AA; 27317 MW; 9EB5D0142CF185A2 CRC64;

Query Match 99.3%; Score 550; DB 2; Length 243;  
 Best Local Similarity 99.1%; Pred. No. 1.4e-50;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASQETLVRRPKPLLLKLLKSVGAQKDTYTMKEVLYLGGYIMTKRLYDEKQOHIVY 60

Db 17 SQIPASEQETLVRRPKPLLLKLLKSVGAQKDTYTMKEVLYLGGYIMTKRLYDEKQOHIVY 76

Qy 61 CSNLLGLDGLFGVPSFVKHRRKIYTMIRNLVNVNQESSDGSSTSVSEN 109

Db 77 CSNLLGLDGLFGVPSFVKHRRKIYTMIRNLVNVNQESSDGSSTSVSEN 125

# RESULT 4

MDM2 HUMAN

ID MDM2 HUMAN

AC Q00987; Q13226; STANDARD; PRT; 491 AA.

AC

DT

DT

DT

DE

DE

DE

GN

OS

OC

OC

OX

RN

RP

RX

RA

RT

RT

RL

RN

RP

RX

RA

RT

RT

RL

RN

RP

RA

RA

RA

RT

RT

RL

RN

RP

RX

RA

RA

RA

RA

RA

RA

RA

RA

RA

RA

RA

RA

RA

RA

RA

RA

RA

RT

RL

RN

RP

RA

RT

RT

RL

RN

Q9UMT8;

01-APR-1993 (Rel. 25, Created)

01-APR-1993 (Rel. 25, Last sequence update)

01-OCT-2004 (Rel. 45, Last annotation update)

Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein Mdm2)

GN Name=MDM2;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN (1)

RP SEQUENCE FROM N.A. (ISOFORM MDM2).

MEDLINE=92310576; PubMed=1614537;

Oliver J.D., Kinzler K.W., Meltzer P.S., George D.L., Vogelstein B.;

"Amplification of a gene encoding a p53-associated protein in human

sarcomas.";

Nature 358:80-83 (1992).

RN (2)

RP SEQUENCE FROM N.A. (ISOFORMS MDM2-A; -B; -C; -D AND -E).

TISSUE=Ovarian carcinoma;

MEDLINE=96313107; PubMed=8705862;

Sigalas I., Calvert A.H., Anderson J.J., Neal D.E., Lunec J.;

"Alternatively spliced mdm2 transcripts with loss of p53 binding

domain sequences: transforming ability and frequent detection in human

cancer.";

Nat. Med. 2:912-917 (1996).

RN (3)

RP SEQUENCE FROM N.A. (ISOFORM MDM2-ALPHA).

MEDLINE=20065171; PubMed=10597303;

Veldhoen N., Metcalfe S., Milner J.;

"A novel exon within the mdm2 gene modulates translation initiation in

vitro and disrupts the p53-binding domain of mdm2 protein.";

Oncogene 18:7026-7033 (1999).

RN (4)

RP SEQUENCE FROM N.A. (ISOFORM MDM2).

Rieder M.J., Livingston R.J., Braun A.C., Montoya M.A., Chung M.-W.,

Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,

Schackwitz W.S., Sherwood J.K., Wittrak L.A., Nickerson D.A.;

"NIHNS-SNPs, environmental genome project, NIHES ES15478, Department

of Genome Sciences, Seattle, WA (URL: <http://egp.gs.washington.edu>).";

Submitted (JUL-2002) to the ENBL/GenBank/DBJ databases.

RN (5)

RP SEQUENCE FROM N.A. (ISOFORM MDM2).

TISSUE=Muscle;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner I., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Gunaratne P.H.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN (6)

RP SEQUENCE OF 6-491 FROM N.A. (ISOFORM MDM2-A1).

Liang H., Atkins H., Abdel-Fattah R., Saeun R., Lunec J.;

"Genomic organisation of the human MDM2 oncogene and relationship to

its alternatively spliced mRNA's.";

Submitted (NOV-1999) to the ENBL/GenBank/DBJ databases.

RN (7)

RP SEQUENCE OF 1-24 FROM N.A.  
 RX MEDLINE=95380270; PubMed=7651818;  
 RA Zauberman A.; Flusberg D.; Haupt Y.; Barak Y.; Oren M.;  
 RT "A functional p53-responsive intronic promoter is contained within the  
 RL human mdm2 gene.";  
 RN Nucleic Acids Res. 23:2584-2592(1995).  
 RP SEQUENCE OF 1-9 FROM N.A.  
 RX MEDLINE=97413643; PubMed=9270029;  
 RA Landers J.E.; Casel S.L.; George D.L.;  
 RT "Translational enhancement of mdm2 oncogene expression in human tumor  
 RL cells containing a stabilized wild-type p53 protein.";  
 RN Cancer Res. 57:3562-3568(1997).  
 RP SEQUENCE OF 301-481 FROM N.A.  
 RX MEDLINE=20542019; PubMed=11087894;  
 RA Taubert H.; Kappler M.; Meyer A.; Bartel F.; Schlott T.;  
 RL Lautenschlaeger C.; Bache M.; Schmidt H.; Wuerl P.;  
 RT "A MboII polymorphism in exon 11 of the human MDM2 gene occurring in  
 RL normal blood donors and in soft tissue sarcoma patients: an indication  
 RL for an increased cancer susceptibility?";  
 RN Mutat. Res. 456:39-44(2000).  
 RP MUTAGENESIS OF CYS-464.  
 RX MEDLINE=98111004; PubMed=9450543;  
 RA Honda R.; Tanaka H.; Yasuda H.;  
 RT "Oncoprotein MDM2 is a ubiquitin ligase E3 for tumor suppressor p53.";  
 RL FEBS Lett. 420:25-27(1997).  
 RP MUTAGENESIS OF CYS-449.  
 RX MEDLINE=20190101; PubMed=10721319;  
 RA Honda R.; Yasuda H.;  
 RT "Activity of MDM2, a ubiquitin ligase, toward p53 or itself is  
 RL dependent on the RING finger domain of the ligase.";  
 RN Oncogene 19:1473-1476(2000).  
 RP MUTAGENESIS.  
 RX MEDLINE=20187618; PubMed=10722742;  
 RA Fang S.; Jensen J.P.; Ludwig R.L.; Vousden K.H.; Weissman A.M.;  
 RT "Mdm2 is a RING finger-dependent ubiquitin protein ligase for itself  
 RL and p53.";  
 RN J. Biol. Chem. 275:8945-8951(2000).  
 RP MUTAGENESIS OF CYS-441 AND CYS-478.  
 RX MEDLINE=20076498; PubMed=10608892;  
 RA Sharp D.A.; Kratowicz S.A.; Sank M.J.; George D.L.;  
 RT "Stabilization of the MDM2 oncoprotein by interaction with the  
 RL structurally related MDMX protein.";  
 RN J. Biol. Chem. 274:38189-38196(1999).  
 RP NUCLEOLAR LOCALIZATION SIGNAL.  
 RX MEDLINE=20173879; PubMed=10707090;  
 RA Lohrum M.A.E.; Ashcroft M.; Kubbutat M.H.G.; Vousden K.H.;  
 RT "Identification of a cryptic nucleolar-localization signal in MDM2.";  
 RL Nat. Cell Biol. 2:179-181(2000).  
 RP PHOSPHORYLATION BY ATM.  
 RX MEDLINE=20079591; PubMed=10611322;  
 RA Khosravi R.; Maya R.; Gottlieb T.; Oren M.; Shiloh Y.; Shkedy D.;  
 RT "Rapid ATM-dependent phosphorylation of MDM2 precedes p53 accumulation  
 RL in response to DNA damage.";  
 RN Proc. Natl. Acad. Sci. U.S.A. 96:14973-14977(1999).  
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 25-109 IN COMPLEX WITH P53.  
 RX MEDLINE=97081050; PubMed=8875929;  
 RA Kussie P.H.; Gorina S.; Marechal V.; Elenbaas B.; Moreau J.;  
 RA Levine A.J.; Pavletich N.P.;  
 RT "Structure of the MDM2 oncoprotein bound to the p53 tumor suppressor  
 RL transactivation domain.";  
 RN Science 274:948-953(1996).  
 RP -1- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and  
 CC apoptosis by binding its transcriptional activation domain.  
 CC Functions as a ubiquitin ligase E3, in the presence of E1 and E2,

CC toward p53 and itself. Permits the nuclear export of p53 and  
 CC targets it for proteasome-mediated proteolysis.  
 CC -1- COFACTOR: Zinc is required for ubiquitin ligase E3 activity.  
 CC -1- SUBUNIT: Binds p53, p73, ARF(P14), ribosomal protein L5 and  
 CC specifically to RNA. Can interact also with retinoblastoma protein  
 CC (RB), E1A-associated protein EP300 and the E2F1 transcription  
 CC factor.  
 CC -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed  
 CC predominantly in the nucleoplasm. Interaction with ARF(P14)  
 CC results in the localization of both proteins to the nucleolus. The  
 CC nucleolar localization signals in both ARF(P14) and MDM2 may be  
 CC necessary to allow efficient nucleolar localization of both  
 CC proteins.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=8;  
 CC Name=Mdm2;  
 CC IsoId=Q00987-1; Sequence=Displayed;  
 CC Name=Mdm2-A;  
 CC IsoId=Q00987-2; Sequence=VSP\_003208;  
 CC Name=Mdm2-A1;  
 CC IsoId=Q00987-3; Sequence=VSP\_003208, VSP\_003214;  
 CC Name=Mdm2-B;  
 CC IsoId=Q00987-4; Sequence=VSP\_003209;  
 CC Name=Mdm2-C;  
 CC IsoId=Q00987-5; Sequence=VSP\_003211;  
 CC Name=Mdm2-D;  
 CC IsoId=Q00987-6; Sequence=VSP\_003210;  
 CC Name=Mdm2-E;  
 CC IsoId=Q00987-7; Sequence=VSP\_003212, VSP\_003213;  
 CC Name=Mdm2-alpha;  
 CC IsoId=Q00987-8; Sequence=VSP\_003207;  
 CC -1- TISSUE SPECIFICITY: Ubiquitous. Isoforms MDM2-A, -B, -C, -D and -E  
 CC are observed in a range of human cancers but absent in normal  
 CC tissues.  
 CC -1- INDUCTION: By DNA damage.  
 CC -1- DOMAIN: Region I is sufficient for binding p53 and inhibiting its  
 CC G1 arrest and apoptosis functions. It also binds p73 and E2F1.  
 CC Region II contains most of a central acidic region required for  
 CC interaction with ribosomal protein L5 and a putative C4-type zinc  
 CC finger. The RING finger domain which coordinates two molecules of  
 CC zinc interacts specifically with RNA whether or not zinc is  
 CC present and mediates the hetero-oligomerization with MDM4. It is  
 CC also essential for its ubiquitin ligase E3 activity toward p53 and  
 CC itself.  
 CC -1- PTM: Phosphorylated in response to ionizing radiation in an ATM-  
 CC dependent manner.  
 CC -1- DISEASE: Seems to be amplified in certain tumors (including soft  
 CC tissue sarcomas, osteosarcomas and gliomas). A higher frequency of  
 CC splice variants lacking p53 binding domain sequences was found in  
 CC late-stage and high-grade ovarian and bladder carcinomas. Four of  
 CC the splice variants show loss of p53 binding.  
 CC -1- MISCELLANEOUS: MDM2 RING finger mutations that failed to  
 CC Query Match 99.3%; Score 550; DB 1; Length 491;  
 CC Best Local Similarity 99.1%; Pred. No. 3.1e-50;  
 CC Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 SQIPASQETLVPRKPLLLKLLKSVGAKQDTYTKKEVLYLQGVYTMKRLYDEKQHHVY 60  
 Db 17 SQIPASQETLVPRKPLLLKLLKSVGAKQDTYTKKEVLYLQGVYTMKRLYDEKQHHVY 76  
 Qy 61 CSNDLLGDLFGVPSFVKHKKIYTMIRYLVVNVNQESSDSGTSVSN 109  
 Db 77 CSNDLLGDLFGVPSFVKHKKIYTMIRYLVVNVNQESSDSGTSVSN 125  
 RESULT 5...  
 AAP35922  
 ID AAP35922 PRELIMINARY; PRT; 491 AA.  
 AC AAP35922;  
 DT 02-MAR-2004 (TREMBLrel. 27, Created)  
 DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)

Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (Mouse).

DE Homo sapiens (Human).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC NCBI\_TaxID=9606;

ON (1)

RP SEQUENCE FROM N.A.

RA Kaline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S., Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y., Phelan M., Farmer A.

RA "Cloning of human full-length cDNAs in BD Creator(TM) System Donor vector."

RT Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.

RL EMBL; BT007258; AAP35922.1; -- F37CE163876BC983 CRC64;

DR EMBL; BT007258; AAP35922.1; -- F37CE163876BC983 CRC64;

SQ SEQUENCE 491 AA; 55232 MW; F37CE163876BC983 CRC64;

Query Match 99.3%; Score 550; DB 2; Length 491;

Best Local Similarity 99.1%; Pred. No. 3.1e-50;

Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SQIPASQETLVPRPKPLLLKLLKSVGAQKDTYTKKVELVYLGQYIMTKRLYDEKQOHIVY 60

DB 17 SQIPASQETLVPRPKPLLLKLLKSVGAQKDTYTKKVELVYLGQYIMTKRLYDEKQOHIVY 76

OY 61 CSNDLLGDLFGVPSFVKHRIYTYMYRNLYVNVNQESSDSGTSVSEN 109

DB 77 CSNDLLGDLFGVPSFVKHRIYTYMYRNLYVNVNQESSDSGTSVSEN 125

RESULT 6

RAAH67077 PRELIMINARY; PRT; 491 AA.

AC AAH67077;

DT 14-APR-2004 (TrEMBLrel. 27, Created)

DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)

DT 14-APR-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

ON (1)

RP SEQUENCE FROM N.A.

RC TISSUE=Muscle;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ussid N.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Feeney J., Helton E., Kettner M., Madan A.C., Rodrigues S., Sanchez A., Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN (2)

RP SEQUENCE FROM N.A.

RC TISSUE=Muscle;

RA Strausberg R.L.

RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC067077; AAH67077.1; --

KW Hypothetical protein.

SQ SEQUENCE 491 AA; 55232 MW; F37CE163876BC983 CRC64;

Query Match 99.3%; Score 550; DB 2; Length 491;

Best Local Similarity 99.1%; Pred. No. 3.1e-50;

Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SQIPASQETLVPRPKPLLLKLLKSVGAQKDTYTKKVELVYLGQYIMTKRLYDEKQOHIVY 60

DB 17 SQIPASQETLVPRPKPLLLKLLKSVGAQKDTYTKKVELVYLGQYIMTKRLYDEKQOHIVY 76

OY 61 CSNDLLGDLFGVPSFVKHRIYTYMYRNLYVNVNQESSDSGTSVSEN 109

DB 77 CSNDLLGDLFGVPSFVKHRIYTYMYRNLYVNVNQESSDSGTSVSEN 125

RESULT 7

MDM2\_CANFA STANDARD; PRT; 487 AA.

ID MDM2\_CANFA

AC P56950; Q95KNS;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Cdm2).

GN Name=MDM2;

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

ON NCBI\_TaxID=9615;

RN (1)

RP SEQUENCE OF 1-484 FROM N.A.

RX MEDLINE=20218866; PubMed=10754200;

RA Nasir L., Burr P.D., McFarlane S.T., Gault E., Thompson H., Arsyale D.J.;

RT "Cloning, sequence analysis and expression of the cDNAs encoding the canine and equine homologues of the mouse double minute 2 (mdm2) proto-oncogene."

RT Cancer Lett. 152:9-13(2000).

RL (2)

RP SEQUENCE FROM N.A. (ISOFORMS MDM2 AND MDM2-ALPHA).

RX MEDLINE=20065171; PubMed=10597303;

RA Veidhoen N., Metcalfe S., Milner J.;

RT "A novel exon within the mdm2 gene modulates translation initiation in vitro and disrupts the p53-binding domain of mdm2 protein."

RL Oncogene 18:7026-7033(1999).

CC -1- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and apoptosis by binding its transcriptional activation domain. Functions as a ubiquitin ligase E3, in the presence of E1 and E2, toward p53 and itself. Permits the nuclear export of p53 and targets it for proteasome-mediated proteolysis (By similarity).

CC -1- COPACITOR: Zinc is required for ubiquitin ligase E3 activity (By similarity).

CC -1- SUBUNIT: Binds p53, p73, ARF(P14), ribosomal protein L5 and specifically to RNA. Can interact also with retinoblastoma protein (RB), E1A-associated protein EP300 and the E2F1 transcription factor (By similarity).

CC -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed predominantly in the nucleoplasm (By similarity).

CC -1- ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=2; Name=Mdm2; IsoId=P56950-1; Sequence=Displayed; IsoId=P56950-2; Sequence=VSP\_003206;

CC -1- TISSUE SPECIFICITY: Isoform Mdm2-alpha is present in lymphoid and testicular tissues.

CC -1- DOMAIN: Region I is sufficient for binding p53 and inhibiting its G1 arrest and apoptosis functions. It also binds p73 and E2F1. Region II contains most of a central acidic region required for interaction with ribosomal protein L5 and a putative C4-type zinc finger. The RING finger domain which coordinates two molecules of zinc interacts specifically with RNA whether or not zinc is present and mediates the hetero-oligomerization with MDM4. It is

OX	NCBI_TaxID=9615;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Liver;
RA	Setoguchi A., Tsujimoto H.;
RL	Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AB031276; BAB11975.1; -
DR	HSSP; Q9UMT8; 1YCR.
DR	GO; GO:0005730; C:nucleolus; ISS.
DR	GO; GO:0005654; C:nucleoplasm; ISS.
DR	GO; GO:0017163; F:negative regulator of basal transcription a. . .; ISS.
DR	GO; GO:0005515; F:protein binding; ISS.
DR	GO; GO:0000122; P:negative regulation of transcription from P. . .; ISS.
DR	InterPro; IPR010984; MDM2.
DR	InterPro; IPR003121; SWIB MDM2.
DR	InterPro; IPR001876; Znf_RanGDP.
DR	InterPro; IPR001841; Znf_ring.
DR	Pfam; PF02201; SWIB; 1.
DR	Pfam; PF00641; zf-RanBP; 1.
DR	SMART; SM00184; RING; 1.
DR	PROSITE; PS01358; ZF_RANBP2_1; 1.
DR	PROSITE; PS01399; ZF_RANBP2_2; 1.
DR	PROSITE; PS50089; ZF_RING_2; 1.
SQ	SEQUENCE 487 AA; 54724 MW; 34FC5CC6A18D7744 CRC64;
	Query Match 97.1%; Score 538; DB 2; Length 487;
	Best Local Similarity 96.3%; Pred. No. 5,9e-49;
	Matches 105; Conservative 2; Mismatches 2; Indels 0; Gaps
QY	1 SQIPASEQETLVRPKLLKLLKSVGAQKDTYTMKEVLYYGQYIMTKRLYDEKQOHIVY 60
DB	17 SQIPASEQETLVRPKLLKLLKSVGAQKDTYTMKEVIFYLQYIMTKRLYDEKQOHIVY 76
QY	61 CNSDLLGLDFGVSPSVKHKRIYMIYRNLVVNNQSSDSGTSVSEN 109
DB	77 CNSDLLGLDFGVSPSVKHKRIYMIYRNLVVNNQHEPDSGTSVSEN 125
RESULT 9	
MDM2_HORSE	
ID	_MDM2_HORSE STANDARD; PRT; 491 AA.
AC	P56951;
DT	30-MAY-2000 (Rel. 39, Created)
DT	30-MAY-2000 (Rel. 39, Last sequence update)
DT	05-JUL-2004 (Rel. 44, Last annotation update)
DE	Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein
DE	Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Edm2).
GN	Name=MDM2;
OS	Equus caballus (Horse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX	NCBI_TaxID=9796;
RP	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=20218866; PubMed=10754200;
RA	Nasir L., Burr P.D., McFarlane S.T., Gault E., Thompson H.,
RA	Argyle D.J.;
RT	"Cloning, sequence analysis and expression of the cDNAs encoding the
RT	canine and equine homologues of the mouse double minute 2 (mdm2)
RT	proto-oncogene.";
RL	Cancer Lett. 152:9-13(2000).
CC	-1- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and
CC	apoptosis by binding its transcriptional activation domain.
CC	Functions as a ubiquitin ligase E3, in the presence of E1 and E2,
CC	toward p53 and itself. Permits the nuclear export of p53 and
CC	targets it for proteasome-mediated proteolysis (By similarity).
CC	-1- COPACATOR: Zinc is required for ubiquitin ligase E3 activity (By
CC	similarity).
CC	-1- SUBUNIT: Binds p53, p73, ARF(P14), ribosomal protein L5 and
CC	specifically to RNA. Can interact also with retinoblastoma protein
CC	(RB), E1A-associated protein EP300 and the E2F1 transcription
CC	factor (By similarity).
CC	-1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed

predominantly in the nucleoplasm (By similarity).  
-!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its G1 arrest and apoptosis functions. It also binds p73 and E2F1. Region II contains most of a central acidic region required for interaction with ribosomal protein L5 and a putative C4-type zinc finger. The RING finger domain which coordinates two molecules of zinc interacts specifically with RNA whether or not zinc is present and mediates the hetero-oligomerization with MDM4. It is also essential for its ubiquitin ligase E3 activity toward p53 and itself (By similarity).  
-!- SIMILARITY: Belongs to the MDM2 / MDM4 family.  
-!- SIMILARITY: Contains 1 RanBP2-type zinc finger.  
-!- SIMILARITY: Contains 1 RING-type zinc finger.  
-!- SIMILARITY: Contains 1 SWIB domain.  
-----  
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-----  
EMBL; AF121140; AAF28866.1; -.  
DR HSSP; Q9UMT8; 1YCR.  
DR InterPro; IPR010984; MDM2.  
DR InterPro; IPR003121; SWIB.  
DR InterPro; IPR001876; Znf\_RanGDP.  
DR InterPro; IPR001841; Znf\_Ring.  
DR Pfam; PF02201; SWIB; 1.  
DR Pfam; PF00641; Zf-RanBP; 1.  
DR SMART; SM00184; RING; 1.  
DR PROSITE; PS01358; ZF\_RANBP2\_1; 1.  
DR PROSITE; PS01099; ZF\_RANBP2\_2; 1.  
DR PROSITE; PS00518; ZF\_RING\_1; FALSE\_NEG.  
DR PROSITE; PS50089; ZF\_RING\_2; 1.  
DR Ligase; Metal-binding; Nuclease protein; Ubl conjugation pathway; Zinc; Zinc-finger.  
KW DOMAIN 27 107 SWIB.  
FT DOMAIN 179 185 Nuclear localization signal (Potential).  
FT DOMAIN 190 202 Nuclear export signal.  
FT DOMAIN 210 304 ARF-binding.  
FT DOMAIN 210 215 Poly-Ser.  
FT DOMAIN 242 331 Region II.  
FT DOMAIN 243 301 Asp/Glu-rich (acidic).  
FT ZN\_FING 299 328 RanBP2-type.  
FT ZN\_FING 438 479 RING-type.  
FT DOMAIN 466 473 Nucleolar localization signal (Potential).  
SQ SEQUENCE 491 AA; 55279 MW; 641E033D5C1DEC39 CRC64;  
Query Match 97.1%; Score 538; DB 1; Length 491;  
Best Local Similarity 96.3%; Pred. No. 5.9e-49;  
Matches 105; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
ID Q7YRZ8 PRELIMINARY; PRT; 491 AA.  
AC Q7YRZ8;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Double minute 2 protein MDM2.  
GN Name=mdm2;  
-----  
1 SOIPASEQETLVPRPKLLKLLKSVGAQKDTYTKVEVLYLQYIMTKRLYDEKQOHIVY 60  
17 SOIPASEQETLVPRPKLLKLLKSVGAQKDTYTKVEVLYLQYIMTKRLYDEKQOHIVY 76  
-----  
61 CSNDLLGLDGFVPSFVKHEKRIYTMIRNVLVWVQSSDGSSTSVSEN 109  
77 CSNDLLGLDGFVPSFVKHEKRIYTMIRNVLVWVQSPSPSGTSVSEN 125  
-----  
RESULT 10  
Q7YRZ8  
ID Q7YRZ8 PRELIMINARY; PRT; 491 AA.  
AC Q7YRZ8;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Double minute 2 protein MDM2.  
GN Name=mdm2;  
-----  
1 SOIPASEQETLVPRPKLLKLLKSVGAQKDTYTKVEVLYLQYIMTKRLYDEKQOHIVY 60  
17 SOIPASEQETLVPRPKLLKLLKSVGAQKDTYTKVEVLYLQYIMTKRLYDEKQOHIVY 76  
-----  
61 CSNDLLGLDGFVPSFVKHEKRIYTMIRNVLVWVQSSDGSSTSVSEN 109  
77 CSNDLLGLDGFVPSFVKHEKRIYTMIRNVLVWVQSPSPSGTSVSEN 125  
-----  
RESULT 11  
Q8WVJ2  
ID Q8WVJ2 PRELIMINARY; PRT; 436 AA.  
AC Q8WVJ2;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE MDM2 protein.  
GN Name=MDM2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21248713; PubMed=11351297;  
RA Tamborini E., Della Torre G., Lavarino C., Azzarelli A., Carpinelli P., Pierotti M.A., Pilotti S.;  
RT "Analysis of the molecular species generated by MDM2 gene amplification in liposarcomas.";  
RL Int. J. Cancer 92:790-796(2001).  
DR EMBL; AF092844; AAL40179.1; -.  
DR HSSP; Q9UMT8; 1YCR.  
DR GO; GO:0005730; C:nucleolus; ISS.  
DR GO; GO:0005654; C:nucleoplasm; ISS.  
DR GO; GO:0017163; F:negative regulator of basal transcription a. . .; ISS.  
DR GO; GO:0005515; F:negative regulator of transcription from P. . .; ISS.  
DR GO; GO:0000122; P:negative regulation of transcription from P. . .; ISS.  
DR InterPro; IPR010984; MDM2.  
DR InterPro; IPR003121; SWIB.  
DR InterPro; IPR001876; Znf\_RanGDP.  
DR InterPro; IPR001841; Znf\_Ring.  
DR Pfam; PF02201; SWIB; 1.  
DR Pfam; PF00641; Zf-RanBP; 1.  
DR SMART; SM00184; RING; 1.

OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
OX NCBI\_TaxID=9685;  
RN [1]  
RP SEQUENCE FROM N.A.  
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB099709; BAC78209.1; -.  
DR GO; GO:0005730; C:nucleolus; ISS.  
DR GO; GO:0005654; C:nucleoplasm; ISS.  
DR GO; GO:0017163; F:negative regulator of basal transcription a. . .; ISS.  
DR GO; GO:0005515; F:negative regulator of transcription from P. . .; ISS.  
DR GO; GO:0000122; P:negative regulation of transcription from P. . .; ISS.  
DR InterPro; IPR003121; SWIB MDM2.  
DR InterPro; IPR001876; Znf\_RanGDP.  
DR InterPro; IPR001841; Znf\_Ring.  
DR Pfam; PF02201; SWIB; 1.  
DR Pfam; PF00641; Zf-RanBP; 1.  
DR SMART; SM00184; RING; 1.  
DR PROSITE; PS01358; ZF\_RANBP2\_1; 1.  
DR PROSITE; PS01099; ZF\_RANBP2\_2; 1.  
DR PROSITE; PS50089; ZF\_RING\_2; 1.  
SQ SEQUENCE 491 AA; 55433 MW; D93E25D638E98934 CRC64;  
Query Match 96.6%; Score 535; DB 2; Length 491;  
Best Local Similarity 95.4%; Pred. No. 1.2e-48;  
Matches 104; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 1 SOIPASEQETLVPRPKLLKLLKSVGAQKDTYTKVEVLYLQYIMTKRLYDEKQOHIVY 60  
17 SOIPASEQETLVPRPKLLKLLKSVGAQKDTYTKVEVLYLQYIMTKRLYDEKQOHIVY 76  
-----  
61 CSNDLLGLDGFVPSFVKHEKRIYTMIRNVLVWVQSSDGSSTSVSEN 109  
77 CSNDLLGLDGFVPSFVKHEKRIYTMIRNVLVWVQSPSPSGTSVSEN 125  
-----  
RESULT 11  
Q8WVJ2  
ID Q8WVJ2 PRELIMINARY; PRT; 436 AA.  
AC Q8WVJ2;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE MDM2 protein.  
GN Name=MDM2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21248713; PubMed=11351297;  
RA Tamborini E., Della Torre G., Lavarino C., Azzarelli A., Carpinelli P., Pierotti M.A., Pilotti S.;  
RT "Analysis of the molecular species generated by MDM2 gene amplification in liposarcomas.";  
RL Int. J. Cancer 92:790-796(2001).  
DR EMBL; AF092844; AAL40179.1; -.  
DR HSSP; Q9UMT8; 1YCR.  
DR GO; GO:0005730; C:nucleolus; ISS.  
DR GO; GO:0005654; C:nucleoplasm; ISS.  
DR GO; GO:0017163; F:negative regulator of basal transcription a. . .; ISS.  
DR GO; GO:0005515; F:negative regulator of transcription from P. . .; ISS.  
DR GO; GO:0000122; P:negative regulation of transcription from P. . .; ISS.  
DR InterPro; IPR010984; MDM2.  
DR InterPro; IPR003121; SWIB.  
DR InterPro; IPR001876; Znf\_RanGDP.  
DR InterPro; IPR001841; Znf\_Ring.  
DR Pfam; PF02201; SWIB; 1.  
DR Pfam; PF00641; Zf-RanBP; 1.  
DR SMART; SM00184; RING; 1.



DR PROSITE, PS01358; ZF\_RANBP2\_1; 1.  
 DR PROSITE, PS50199; ZF\_RANBP2\_2; 1.  
 DR PROSITE, PS50089; ZF\_RING\_2; 1.  
 SQ SEQUENCE 436 AA; 49248 MW; 3CBF55E98BC4203A CRC64;

Query Match 90.3%; Score 500; DB 2; Length 436;  
 Best Local Similarity 93.3%; Pred. No. 6.1e-45;  
 Matches 98; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVPRPLLLKLLKSGVGAQKDTYTMKEVLYLQGYIMTKRLYDEKQOHIVY 60  
 Db 17 SQIPASEQETLVPRPLLLKLLKSGVGAQKDTYTMKEVLYLQGYIMTKRLYDEKQOHIVY 76

QY 61 CSNDLLGLDGLFGVPSFVSEHKRIYMYIRNLVNVNQSSDSGTS 105  
 Db 77 CSNDLLGLDGLFGVPSFVSEHKRIYMYIRNLVNVNQSSDSGTS 121

RESULT 12

MDM2\_MOUSE

ID MDM2\_MOUSE STANDARD; PRT; 489 AA.  
 AC P23804; Q61040; Q64330;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) [p53-binding protein  
 Mdm2] (Oncoprotein Mdm2) (Double minute 2 protein).  
 GN Name=Mdm2;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM MDM2-P90).  
 RX MEDLINE=91224107; PubMed=2026149;  
 RA Fakharzaden S.S., Trusko S.P., George D.L.;  
 RT "Tumorigenic potential associated with enhanced expression of a gene  
 that is amplified in a mouse tumor cell line.";  
 RL EMBO J. 10:1565-1569 (1991).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM MDM2-P90).  
 RC STRAIN=129/Sv;  
 RX MEDLINE=97074674; PubMed=8917101;  
 RA Jones S.N., Ansari-Lari M.A., Hancock A.R., Jones W.J., Gibbs R.A.,  
 RA Donehower L.A., Bradley A.;  
 RT "Genomic organization of the mouse double minute 2 gene.";  
 RL Gene 175:209-213 (1996).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM MDM2-P90).  
 RC STRAIN=129/Sv;  
 RX MEDLINE=96299630; PubMed=8660994;  
 RA de Oca Luna R.M., Tabor A.D., Eberspaecher H., Hulboy D.L.,  
 RA Worth L.L., Colman M.S., Finlay C.A., Lozano G.;  
 RT "The organization and expression of the mdm2 gene.";  
 RL Genomics 33:352-357 (1996).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORMS MDM2-P90 AND MDM2-P76).  
 RX MEDLINE=91751199; PubMed=10075719;  
 RA Saucedo L.J., Myers C.D., Perry M.E.;  
 RT "Multiple murine double minute gene 2 (MDM2) proteins are induced by  
 ultraviolet light.";  
 RL J. Biol. Chem. 274:8161-8168 (1999).  
 RN [5]  
 RP NUCLEOLAR LOCALIZATION SIGNAL.  
 RX MEDLINE=20180080; PubMed=10713175;  
 RA Weber J.D., Kuo M.-L., Bothner B., Digiammarino E.L., Kriwacki R.W.,  
 RA Roussel M.F., Sherr C.J.;  
 RT "Cooperative signals governing ARF-mdm2 interaction and nucleolar  
 localization of the complex.";  
 RL Mol. Cell. Biol. 20:2517-2528 (2000).  
 RN [6]  
 RP PHOSPHORYLATION BY ATM.  
 RX MEDLINE=20079591; PubMed=10611322;

RA Khosravi R., Maya R., Gottlieb T., Oren M., Shiloh Y., Shkedy D.;  
 RT "Rapid ATM-dependent phosphorylation of MDM2 precedes p53 accumulation  
 in response to DNA damage.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 96:14973-14977 (1999).  
 CC -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and  
 apoptosis by binding its transcriptional activation domain.  
 CC Functions as a ubiquitin ligase E3, in the presence of E1 and E2,  
 toward p53 and itself. Permits the nuclear export of p53 and  
 targets it for proteasome-mediated proteolysis.  
 CC -!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity.  
 CC -!- SUBUNIT: Binds p53, p73, ARF (P14), ribosomal protein L5 and  
 specifically to RNA. Can interact also with retinoblastoma protein  
 (RB), E1A-associated protein E1300 and the E2F1 transcription  
 factor.  
 CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed  
 predominantly in the nucleoplasm. Interaction with ARF (P14)  
 results in the localization of both proteins to the nucleolus. The  
 nucleolar localization signals in both ARF (P14) and MDM2 may be  
 necessary to allow efficient nucleolar localization of both  
 proteins.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=Mdm2-p90;  
 CC IsoId=P23804-1; Sequence=Displayed;  
 CC Note=Isoform Mdm2-p76 can also be produced by alternative  
 initiation at Met-50 of isoform Mdm2-p90, but is produced more  
 efficiently by alternative splicing;  
 CC Name=Mdm2-p76;  
 CC IsoId=P23804-2; Sequence=VSP\_003215;  
 CC Note=Does not bind to p53;  
 CC Event=Alternative initiation;  
 CC Comment=2 isoforms, Mdm2-p90 (shown here) and Mdm2-p76, are  
 produced by alternative initiation at Met-1 and Met-50. Isoform  
 Mdm2-p76 is produced more efficiently by alternative splicing.  
 CC -!- TISSUE SPECIFICITY: Ubiquitously expressed at low-level throughout  
 embryo development and in adult tissues. MDM2-p90 is much more  
 abundant than MDM2-p76 in testis, brain, heart, and kidney, but in  
 the thymus, spleen, and intestine, the levels of the MDM2 proteins  
 are roughly equivalent.  
 CC -!- INDUCTION: By UV light.  
 CC -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its  
 G1 arrest and apoptosis functions. It also binds p73 and E2F1.  
 CC Region II contains most of a central acidic region required for  
 interaction with ribosomal protein L5 and a putative C4-type zinc  
 finger. The RING finger domain which coordinates two molecules of  
 zinc interacts specifically with RNA whether or not zinc is  
 present and mediates the hetero-oligomerization with MDM4. It is  
 also essential for its ubiquitin ligase E3 activity toward p53 and  
 itself.  
 CC -!- PTM: Phosphorylated in response to ionizing radiation in an ATM-  
 dependent manner.  
 CC -!- DISEASE: The gene for this protein is amplified in a mouse tumor  
 cell line.  
 CC -!- SIMILARITY: Belongs to the MDM2 / MDM4 family.  
 CC -!- SIMILARITY: Contains 1 RanBP2-type zinc finger.  
 CC -!- SIMILARITY: Contains 1 RING-type zinc finger.  
 CC -!- SIMILARITY: Contains 1 SWIB domain.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; X58876; CAA41684.1; -;  
 DR EMBL; U40145; AAA91167.1; -;  
 DR EMBL; U47944; AAB09030.1; -;  
 DR EMBL; U47935; AAB09030.1; JOINED.  
 DR EMBL; U47936; AAB09030.1; JOINED.  
 DR EMBL; U47937; AAB09030.1; JOINED.  
 DR EMBL; U47938; AAB09030.1; JOINED.



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RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Baka S.A., Lequellano N.J., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Rohak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalski U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Mouse;
RA Strausberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kohji Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Oheato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takagawa-Akai H., Takeda Y., Tanaka T.,
RA Tonaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK004719; BAB31502.1; -
DR EMBL; BC050902; ANH50902.1; -
DR EMBL; AC088638; BAC40470.1; -
DR HSSP; Q9UNT8; 1YCR.
DR MGD; MGI:96952; Mdm2.
DR GO; GO:0005730; C:nucleolus; IDA.
DR GO; GO:0005515; P:protein binding; IPI.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IDA.
DR GO; GO:0030163; P:protein catabolism; IDA.
DR GO; GO:0016567; P:protein ubiquitination; IDA.
DR GO; GO:0007089; P:traversing start control point of mitotic c. . .; IDA.
DR InterPro; IPR010984; MDM2.
DR InterPro; IPR003121; SWIB_MDM2.
DR InterPro; IPR001876; Znf_RangBP.
DR Pfam; PF02201; SWIB; 1.
DR Pfam; PF06641; ZF-RanBP; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01358; ZF_RANBP2_1; 1.
DR PROSITE; PS01359; ZF_RANBP2_2; 1.
DR PROSITE; PS00089; ZF_RING_2; 1.
SQ SEQUENCE 489 AA; 54557 MW; 4ABF489A82038DF4 CRC64;

Query Match 88.5%; Score 490.5; DB 2; Length 489;
Best Local Similarity 87.2%; Pred. No. 7.3e-44;
Matches 95; Conservative 8; Mismatches 3; Indels 3; Gaps 1;

Qy 1 SQIPASQETLVPRPKPLLLKLLKSVGAQKQYTTWKVELVYLGQYIMTKRLYDEKQKHIVY 60
Db 17 SQIPASEQETLVPRPKPLLLKLLKSVGAQNDYTTWKELIFYGQYIMTKRLYDEKQKHIVY 76
Qy 61 CSNDLLGDLFGVPSFSVKEHRKIYMTIYRNVLV 109

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Db 77 CSNDLLGDLFGVPSFSVKEHRKIYMTIYRNVLVAVSQQ---DSGTSLSES 122
RESULT 14
Q8WYJ3 PRELIMINARY; PRT; 118 AA.
AC Q8WYJ3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MDM2 protein (Fragment).
GN Name=MDM2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21248713; PubMed=11351297;
RA Tamborini E., Della Torre G., Lavarino C., Azzarelli A.,
RA Carpinelli P., Pierotti M.A., Pilotti S.;
RT "Analysis of the molecular species generated by MDM2 gene
RT amplification in liposarcomas";
RL Int. J. Cancer 92:790-796 (2001).
DR EMBL; AF092843; AAL40178.1; -
DR GO; GO:0005634; C:nucleus; IEA.
DR InterPro; IPR010984; MDM2.
DR InterPro; IPR003121; SWIB_MDM2.
DR Pfam; PF02201; SWIB; 1.
DR NON_TER 118 118
SQ SEQUENCE 118 AA; 13536 MW; D74ADBAA83D8841B CRC64;

Query Match 85.4%; Score 473; DB 2; Length 118;
Best Local Similarity 98.9%; Pred. No. 1.1e-42;
Matches 92; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASQETLVPRPKPLLLKLLKSVGAQKQYTTWKVELVYLGQYIMTKRLYDEKQKHIVY 60
Db 17 SQIPASEQETLVPRPKPLLLKLLKSVGAQKQYTTWKELIFYGQYIMTKRLYDEKQKHIVY 76
Qy 61 CSNDLLGDLFGVPSFSVKEHRKIYMTIYRNVLV 93
Db 77 CSNDLLGDLFGVPSFSVKEHRKIYMTIYRNVLV 109

RESULT 15
MDM2_MESAU
ID _MDM2_MESAU STANDARD; PRT; 466 AA.
AC Q60524;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein
DE Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (fragment).
GN Name=MDM2;
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Pancreas;
RX MEDLINE=95300112; PubMed=7780969;
RA Chang K.W., Laconi S., Mangold K.A., Hubchak S., Scarpelli D.G.;
RT "Multiple genetic alterations in hamster pancreatic ductal
RT adenocarcinomas.";
RL Cancer Res. 55:2560-2568 (1995).
CC -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and
CC apoptosis by binding its transcriptional activation domain.
CC Functions as a ubiquitin ligase E3, in the presence of E1 and E2,
CC toward p53 and itself. Permits the nuclear export of p53 and

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OM protein - protein search, using sw model

Run on: January 27, 2005, 17:45:30 ; Search time 80.8 Seconds  
(without alignments)  
483.929 Million cell updates/sec

Title: US-10-822-254-8

Perfect score: 554

Sequence: 1 SQIPASQETLVRPKPLLK.....NLVVNQSSDSSTSVSEN 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	550	99.3	284	2	AAR75494 Human dou
2	550	99.3	284	2	AAR75397 Human dou
3	550	99.3	491	2	AAR42175 Human MDM
4	550	99.3	491	2	AAR76696 Human MDM
5	550	99.3	491	2	AAR07887 Human MDM
6	550	99.3	491	2	AAW15463 Human MDM
7	550	99.3	491	2	AAW13380 Human MDM
8	550	99.3	491	2	AAW13600 Murine do
9	550	99.3	491	2	AAW48241 Human MDM
10	550	99.3	491	2	AAW57241 Human MDM
11	550	99.3	491	2	AAW42879 Amino aci
12	550	99.3	491	2	AAW42971 Amino aci
13	550	99.3	491	2	AAW94304 Human MDM
14	550	99.3	491	3	AAW96567 MDM2 onco
15	550	99.3	491	4	AAW48284 Human MDM
16	550	99.3	491	5	AAW22654 Human Rin
17	550	99.3	491	5	AAW22698 Human Rin
18	550	99.3	491	5	AAW25913 Human dou
19	550	99.3	491	5	AAW015376 Human Dm2
20	550	99.3	491	7	ADD21815 Human mdm
21	550	99.3	491	7	ADL23893 Human Pro
22	550	99.3	491	8	ADL23893 Human E3
23	550	99.3	491	8	ADO52353 Human p53
24	550	99.3	491	8	ADP12593 Protein e
25	550	99.3	491	8	ADN71936 MDM2 prot

26	550	99.3	491	8	ADQ19417 Human sof
27	550	99.3	1171	4	AAU32421 Novel hum
28	533.5	96.3	216	3	AA08846 A human M
29	524.5	94.7	522	7	ADJ95152 Novel NOV
30	524.5	94.7	522	7	ADJ95154 Novel NOV
31	490.5	88.5	489	2	AAW42176 Murine MD
32	490.5	88.5	489	2	AAW76697 Mouse MDM
33	490.5	88.5	489	2	AAW07888 Murine MD
34	490.5	88.5	489	2	AAW15464 Murine MD
35	490.5	88.5	489	2	AAW48242 Mouse MDM
36	490.5	88.5	489	2	AAW57246 Mouse MDM
37	490.5	88.5	489	2	AAW42997 Amino aci
38	490.5	88.5	489	2	AAW42972 Amino aci
39	490.5	88.5	489	2	AAW94305 Mouse MDM
40	490.5	88.5	489	5	AAE25914 Mouse dou
41	490.5	88.5	489	5	ABB57099 Mouse isc
42	490.5	88.5	489	5	AAO15375 Mouse Dm2
43	490.5	88.5	489	7	ADD21816 Mouse mdm
44	490.5	88.5	489	7	ADG61560 Rat Prote
45	352	63.5	227	2	AAW75495 Human dou

## ALIGNMENTS

### RESULT 1

AAW75494  
ID AAR75494 standard; protein; 284 AA.

XX AAR75494;

AC AAR75494;

XX 02-FEB-1996 (first entry)

XX Human double minute 2 (hdm-2) antibody-binding region fragment 1.

XX Human double minute gene 2; hdm-2; antibody binding region; antigen;

KW cancer; sarcoma; rhabdomyosarcoma; diagnosis; immunoassay.

OS Homo sapiens.

XX Key Location/Qualifiers

XX Region 1..284

XX DE4339533-A1. /note= "amino acids 1-284 of hdm-2 gene product"

XX 14-JUN-1995.

XX 19-NOV-1993; 93DE-04339533.

XX 19-NOV-1993; 93DE-04339533.

XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX Zentgraf H, Klein R, Frey M, Martens R;

XX WPI; 1995-216248/29.

XX N-PSDB; AAQ92515.

XX Detection of human double minute gene 2 (hdm-2) antibodies - by incubation with new hdm-2 or antibody-binding hdm-2 fragments; useful in the detection of specific cancers.

XX Claim 11; Fig 1; 12pp; German.

XX Fragments contg. amino acids 1-284, 58-284 and 58-491 of the hdm-2 (human double minute 2) gene product are claimed. The overlapping proteins and fragments contain binding regions for hdm-2- specific antibodies and are useful for identifying such antibodies in a claimed immunoassay method.

XX The presence of anti-hdm-2 antibodies is diagnostic of certain forms of cancer, e.g. rhabdomyosarcoma

XX Sequence 284 AA;

SQ

Query Match 99.3%; Score 550; DB 2; Length 284;  
 Best Local Similarity 99.1%; Pred. No. 3.6e-62;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVY 60  
 Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 109  
 Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 125

## RESULT 2

AAR75397  
 ID AAR75397 standard; protein; 284 AA.

XX AC AAR75397;

XX DT 25-MAR-2003 (revised)

XX DT 25-JAN-1996 (first entry)

XX DE Human double minute 2 (hdm-2) antibody-binding region fragment 1.

XX KW Human double minute gene 2; hdm-2; antibody binding region; antigen;  
 cancer; sarcoma; rhabdomyosarcoma; diagnosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
 XX FT Region 1. 284  
 XX FT /note= "amino acids 1-284 of hdm-2 gene product"

XX EN DE4345249-A1.  
 XX XX 24-MAY-1995.

XX PD 19-NOV-1993; 93DE-04345249.  
 XX PF 19-NOV-1993; 93DE-04339533.

XX PR 19-NOV-1993; 93DE-04339533.  
 XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX PI Zentgraf H, Klein R, Frey M, Martens R;

XX WPI; 1995-195167/26.  
 DR N-PSDB; AAQ87261.

XX PT New hdm-2 fragments contg. antibody binding region - used to detect  
 specific antibodies for diagnosis of cancers, also new DNA sequences  
 encoding them.

XX PS Claim 2; Fig 1; 11pp; German.

XX CC Fragments contg. amino acids 1-284, 58-284 and 58-491 of the hdm-2 (human  
 double minute 2) gene product are claimed. The overlapping protein  
 fragments contain binding regions for hdm-2 specific antibodies and are  
 useful for identifying such antibodies. The presence of anti-hdm-2  
 antibodies is diagnostic of certain forms of cancer, e.g.  
 rhabdomyosarcoma. (Updated on 25-MAR-2003 to correct PF field.)

XX SQ Sequence 284 AA;

Query Match 99.3%; Score 550; DB 2; Length 284;  
 Best Local Similarity 99.1%; Pred. No. 3.6e-62;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVY 60  
 Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 109

Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 125

## RESULT 3

AAR42175  
 ID AAR42175 standard; protein; 491 AA.

XX AC AAR42175;

XX DT 25-MAR-2003 (revised)

XX DT 05-MAY-1994 (first entry)

XX DE Human MDM2.

XX KW p53 gene; tumour suppressor gene; regulation; cellular proliferation;  
 cellular transformation; carcinoma; human; tumour; MDM2; inhibition;  
 gene amplification.

XX OS Homo sapiens.

XX EN WO9320238-A2.

XX PD 14-OCT-1993.

XX PF 07-APR-1993; 93WO-US003199.

XX PR 07-APR-1992; 92US-00867840.

XX PR 23-JUN-1992; 92US-00903103.

XX PA (UYJO) UNIV JOHNS HOPKINS.

XX PI Burrell M, Hill DE, Kinzler KW, Vogelstein B;

XX WPI; 1993-336944/42.  
 DR N-PSDB; AAQ49891.

XX PT Diagnosing neoplasia from amplification of MDM2 gene - or elevated gene  
 expression, also new DNA, MDM2 protein, antibodies and treatment of  
 sarcoma by inhibiting MDM2 expression.

XX PS Claim 19; Fig 1; 75pp; English.

XX CC This sequence is encoded by the MDM2 gene. Amplification of the MDM2 gene  
 is diagnostic of neoplasia or the potential for neoplasia. The protein  
 encoded by this gene interacts with the product of the p53 gene. p53 is a  
 tumour-suppressor gene and encodes a protein which appears to be a member  
 of a group of proteins which regulate normal cellular proliferation and  
 suppression-of-cellular-transformation. Inactivation of the p53 gene has  
 been implicated in the formation, or progression of a wide variety of  
 carcinoma. Polypeptides containing at least amino acids 13-41 of p53, or  
 the DNA encoding these may be used to inhibit the growth of tumour cells  
 containing MDM2 gene amplification. (Updated on 25-MAR-2003 to correct PN  
 field.)

XX SQ Sequence 491 AA;

Query Match 99.3%; Score 550; DB 2; Length 491;  
 Best Local Similarity 99.1%; Pred. No. 7.6e-62;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVY 60  
 Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 109  
 Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 125

## RESULT 4

AAR76696  
 ID AAR76696 standard; protein; 491 AA.

```

XX AC AAR76696;
XX AC 16-OCT-2003 (revised)
XX DT 01-NOV-1995 (first entry)
XX DE Human MDM2 protein.
XX KW MDM2; sarcoma; diagnostic; DNA probe.
XX OS Homo sapiens; (cell line CaCo-2).
XX PN US5420263-A.
XX PD 30-MAY-1995.
XX PF 07-APR-1993; 93US-00044619.
XX PR 07-APR-1992; 92US-00867840.
XX PR 23-JUN-1992; 92US-00903103.
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX PI Vogelstein B, Kinzler KW;
XX DR WPI; 1995-206312/27.
XX DR N-PSDB; AAQ94589.
XX PT New human MDM2 cDNA - used to develop prods. for use in the diagnosis and
XX PT treatment of tumours.
XX PS Claim 1; Col 23-26; 34pp; English.
XX CC The human MDM2 gene is genetically altered (i.e. amplified) in human
XX CC tumour cells. The human MDM2 protein binds to human p53 and allows the
XX CC cell to escape from p53-regulated growth. Detecting that the gene has
XX CC become amplified or detecting increased gene product expression (using
XX CC probes, proteins, antibodies and inhibitors) allows diagnosis and therapy
XX CC of cancers such as colorectal carcinoma, lung cancer and chronic
XX CC myelogenous leukaemia. (Updated on 16-OCT-2003 to standardise OS field)
XX SQ Sequence 491 AA;

Query Match 99.3%; Score 550; DB 2; Length 491;
Best Local Similarity 99.1%; Pred. No. 7.6e-62;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVPRPKPLLLKLLKSVGAQKDTYTMKEVLYYLQYIMTKRLYDEKQOHIVY 60
Db 17 SQIPASEQETLVPRPKPLLLKLLKSVGAQKDTYTMKEVLYYLQYIMTKRLYDEKQOHIVY 76
Qy 61 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 109
Db 77 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 125

RESULT 5
AAW07887
ID AAW07887 standard; protein; 491 AA.
XX AC AAW07887;
XX DT 25-MAR-2003 (revised)
XX DT 28-JAN-1997 (first entry)
XX DE Human MDM-2, involved in tumour-development.
XX KW p53; MDM-2; binding-inhibitor; identification; tumour; cancer; neoplasia;
XX KW antibody fusion protein; therapy.
XX OS Homo sapiens.
XX PH Key Location/Qualifiers

```

```

FT Modified-site 166. .169
FT /label= phosphorylation_site
FT /note= "potential casein kinase II phosphorylation site"
FT Binding-site 181. .185
FT /label= nuclear_localisation_signal
FT Modified-site 192. .195
FT /label= phosphorylation_site
FT /note= "potential casein kinase II phosphorylation site"
FT Domain 223. .274
FT /label= acid_activation_domain
FT Modified-site 269. .272
FT /label= phosphorylation_site
FT /note= "potential casein kinase II phosphorylation site"
FT Modified-site 290. .293
FT /label= phosphorylation_site
FT /note= "potential casein kinase II phosphorylation site"
FT Domain 305. .322
FT /label= metal_binding_site
FT Domain 461. .478
FT /label= metal_binding_site
XX US5550023-A.
XX PN 27-AUG-1996.
XX PD 18-MAY-1994; 94US-00245500.
XX PF 07-APR-1992; 92US-00867840.
XX PR 23-JUN-1992; 92US-00903103.
XX PR 07-APR-1993; 93US-00044619.
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX PI Vogelstein B, Kinzler KW;
XX WPI; 1996-401591/40.
XX N-PSDB; AAT45151.
XX Identification of cpds. interfering with human MDM2/p53 binding - useful
XX as therapeutic agents to treat human neoplastic cells.
XX Claim 26; Col 25-28; 36pp; English.
XX AAW07887 represents human MDM-2 derived from a human colon carcinoma cell
XX line, CaCo-2, cDNA library. The MDM-2 protein is used in a method for
XX identifying compounds that interfere with the binding of p53 and MDM-2.
XX In binding the p53 protein, the MDM-2 protein releases a cell from p53-
XX regulated growth, allowing cancers to develop. Therefore compounds
XX identified as interfering with the binding of MDM-2 to p53 are
XX potentially useful in the treatment of human neoplastic cells. In the
XX method pref. one or both of the proteins is a fusion protein esp. with an
XX antibody or antibody fragment which aids separation and identification.
XX (Updated on 25-MAR-2003 to correct PF field.)
XX SQ Sequence 491 AA;

Query Match 99.3%; Score 550; DB 2; Length 491;
Best Local Similarity 99.1%; Pred. No. 7.6e-62;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVPRPKPLLLKLLKSVGAQKDTYTMKEVLYYLQYIMTKRLYDEKQOHIVY 60
Db 17 SQIPASEQETLVPRPKPLLLKLLKSVGAQKDTYTMKEVLYYLQYIMTKRLYDEKQOHIVY 76
Qy 61 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 109
Db 77 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 125

RESULT 6
AAW15463
ID AAW15463 standard; protein; 491 AA.
XX

```

AC AAW15463;  
 DT 25-MAR-2003 (revised)  
 DT 18-JUN-1997 (first entry)  
 XX Human MDM2.  
 XX Human; MDM2 protein; antibody; detection; cancer; diagnosis;  
 KW p53-regulated growth.  
 KW  
 XX Homo sapiens.  
 OS  
 XX US5618921-A.  
 XX PN  
 XX PD 08-APR-1997.  
 XX PF 17-FEB-1995; 95US-00390479.  
 XX PR 07-APR-1992; 92US-00867840.  
 PR 23-JUN-1992; 92US-00903103.  
 PR 07-APR-1993; 93US-00044619.  
 XX  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 XX Vogelstein B, Kinzler KW, Burrell M, Hill DE;  
 XX WPI; 1997-225474/20.  
 DR N-PSDB; AAT66410.  
 XX  
 XX Antibodies specific for human MDM2 protein - for diagnosis of cancer.  
 XX  
 XX Claim 1; Col 19-24; 35pp; English.  
 XX  
 XX This sequence represents the human MDM2 protein. Antibodies that  
 CC specifically bind to human MDM2 protein may be used for detecting  
 CC elevated expression of the MDM2 gene in a human tissue or body fluid  
 CC sample, esp. for cancer diagnosis. The antibodies may be used to  
 CC interfere with the binding of p53 to MDM2. Elevated levels of MDM2 appear  
 CC to sequester p53 and allow the cell to escape from p53-regulated growth.  
 CC (Updated on 25-MAR-2003 to correct PF field.)  
 XX  
 XX Sequence 491 AA;  
 SQ  
 Query Match 99.3%; Score 550; DB 2; Length 491;  
 Best Local Similarity 99.1%; Pred. No. 7.6e-62;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQOHIVY 60  
 Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQOHIVY 76  
 QY 61 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVVNQOESSDSGTSVSEN 109  
 Db 77 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVVNQOESSDSGTSVSEN 125  
 RESULT 7  
 AAW13380  
 ID AAW13380 standard; protein; 491 AA.  
 XX  
 AC AAW13380;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 05-JUN-1997 (first entry)  
 XX  
 XX Human MDM2 protein.  
 DE  
 XX Human; MDM2; CaCo-2; colonic; carcinoma; probe; detection; amplification;  
 KW elevation; expression; diagnosis; neoplasia; neoplastic transformation;  
 KW sarcoma; colorectal; lung cancer; chronic myelogenous leukaemia.  
 XX  
 XX Homo sapiens.  
 OS  
 XX

PN US5606044-A.  
 XX  
 XX 25-FEB-1997.  
 XX  
 XX 17-FEB-1995; 95US-00390546.  
 XX  
 XX 07-APR-1992; 92US-00867840.  
 PR 23-JUN-1992; 92US-00903103.  
 PR 07-APR-1993; 93US-00044619.  
 XX  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 XX Kinzler KW, Vogelstein B, Hill DE, Burrell M;  
 XX WPI; 1997-153623/14.  
 DR N-PSDB; AAT62065.  
 XX  
 XX Detection of amplification of human MDM2 gene - useful for diagnosis of  
 PT neoplasia or potential neoplastic transformation.  
 PT  
 XX Example 1; Col 21-24; 35pp; English.  
 XX  
 XX The present sequence is the human MDM2 protein, the cDNA for which was  
 CC isolated from a human CaCo-2 colonic carcinoma cell cDNA library using a  
 CC murine MDM2 cDNA probe. The MDM2 cDNA can be used as a probe to detect  
 CC the amplification or elevated expression of a human MDM2 gene, which is  
 CC diagnostic of neoplasia or the potential for neoplastic transformation,  
 CC useful for the detection of, e.g. sarcomas, colorectal carcinoma, lung  
 CC cancer and chronic myelogenous leukaemia. (Updated on 25-MAR-2003 to  
 CC correct PF field.)  
 XX  
 XX Sequence 491 AA;  
 SQ  
 Query Match 99.3%; Score 550; DB 2; Length 491;  
 Best Local Similarity 99.1%; Pred. No. 7.6e-62;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQOHIVY 60  
 Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQOHIVY 76  
 QY 61 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVVNQOESSDSGTSVSEN 109  
 Db 77 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVVNQOESSDSGTSVSEN 125  
 RESULT 8  
 AAW13600  
 ID AAW13600 standard; protein; 491 AA.  
 XX  
 AC AAW13600;  
 XX  
 XX 16-JAN-1998 (first entry)  
 DT  
 XX Murine double minute 2 protein sequence.  
 DE  
 XX Mouse; Mdm2; murine double minute; phosphoprotein; binding; modulation;  
 KW tumour suppressor; p53; oncogene; cell cycle arrest; p107; antagonist;  
 KW inhibition; transcription factor; adenocarcinoma; colon; cancer; breast;  
 KW lung; stomach; myeloid leukaemia; lymphoma; hyperproliferative;  
 KW restenosis.  
 XX  
 XX Mus musculus.  
 OS  
 XX WO9709343-A2.  
 XX PN  
 XX 13-MAR-1997.  
 PD  
 XX 02-SEP-1996; 96WO-FR001340.  
 PF  
 XX 04-SEP-1995; 95FR-00010331.  
 PR  
 XX (RHON ) RHONE POULENC RORER SA.  
 PA



PA (INRM ) INST NAT SANTE & RECH MEDICALE.  
XX  
PI Tocque B, Dube-Peterszman M, Wasylyk B;  
XX  
DR WPI; 1997-192837/17.  
XX N-PSDB; AAT61637.  
XX  
PT Treating cancer with antagonist of oncogenic activity of protein Mdm2 -  
PT or nucleic acid encoding an antagonist, also viral vectors contg. this  
PT nucleic acid.  
XX  
PS Claim 2; Page 26-30; 43pp; French.  
XX  
CC This is the amino acid sequence of the mouse Mdm2 (murine double minute-  
CC 2) protein, a 90 kd phosphoprotein which binds and modulates the activity  
CC of the tumour suppressor protein p53. It has now been shown that the mdm2  
CC protein itself has oncogenic properties, especially in a p53-null  
CC background. Mdm2 is observed to unblock cell cycle arrest in G1 caused by  
CC over-expression of the p107 protein. This is especially done by the  
CC region covering amino acid 1-134. The invention therefore relates to  
CC antagonists able to inhibit the oncogenic activity of mdm2. These include  
CC fragments of the p53 protein, especially amino acids 1-52, 1-41, 6-41, 16  
CC -25 or 18-23 (AAW13602-6), or fragments of transcription factors e.g.  
CC TFII, TBP or TAF250, which bind amino acids 1-134 of mdm2. Other  
CC inhibitors include compounds which disrupt binding to region 135-491 of  
CC mdm2, e.g. Rb, L5 or the transcription factor E2F. The antagonists are  
CC used to treat e.g. adenocarcinoma of the colon; cancer of the breast,  
CC lung or stomach; myeloid leukaemia; B cell lymphoma, or other  
CC hyperproliferative conditions such as restenosis  
XX  
SQ Sequence 491 AA;  
Query Match 99.3%; Score 550; DB 2; Length 491;  
Best Local Similarity 99.1%; Pred. No. 7.6e-62;  
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLYLQYIMTKRLYDEKQOHIVY 60  
DB 17 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLYLQYIMTKRLYDEKQOHIVY 76  
QY 61 CSNDLLGLDGLFGVPFSVKEHRKIYTMIRNLLVNVNQESSDGSSTSVSEN 109  
DB 77 CSNDLLGLDGLFGVPFSVKEHRKIYTMIRNLLVNVNQESSDGSSTSVSEN 125  
RESULT 9  
AAW48241  
ID AAW48241 standard; protein; 491 AA.  
XX  
AC AAW48241;  
XX  
DT 18-JUN-1998 (first entry)  
XX  
DE Human MDM2.  
XX  
KW Human; MDM2; hMDM2; tumour; cancer; diagnosis; neoplastic disease;  
KW sarcoma; liposarcoma; malignant fibrous histiocytoma; osteosarcoma.  
XX  
OS Homo sapiens.  
XX  
PN US5736338-A.  
XX  
PD 07-APR-1998.  
XX  
PF 17-FEB-1995; 95US-00390517.  
XX  
PR 07-APR-1992; 92US-00867840.  
PR 23-JUN-1992; 92US-00903103.  
PR 07-APR-1993; 93US-00044619.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Vogelstein B, Kinzler KW, Hill DE, Burrell M;  
XX  
DR WPI; 1998-321574/28.  
XX N-PSDB; AAV28876.  
XX  
PT Inhibiting growth of tumour cells having MDM2 gene amplification - with  
PT p53 protein fragment.  
XX  
PS Claim 1; Col 23-28; 40pp; English.  
XX  
CC A method has been developed for inhibiting the growth of tumour cells  
CC containing a human MDM2 gene amplification. The method comprises treating  
CC the tumour cells with a DNA molecule that expresses a polypeptide capable  
CC of binding to human MDM2 protein. The present sequence represents human  
CC MDM2 protein. The present invention describes three preferred  
CC polypeptides for binding human MDM2: (1) the polypeptide comprises amino

CC acids 1-50 of p53 (see AAW57240); (2) the polypeptide comprises amino  
 CC acids 13-41 of p53 (see AAW57240) and at least none additional p53  
 CC residues on the N- or C-terminal side, provided that the polypeptide  
 CC lacks the homooligomerisation domain of p53; (3) the polypeptide  
 CC comprises amino acids 13-41 of p53 (see AAW57241) and at least nine  
 CC additional p53 residues on the N- or C-terminal side, provided that the  
 CC polypeptide lacks amino acids 138-393 of p53. Some malignant fibrous  
 CC histiocytomas and liposarcomas have an MDM2 gene amplification, so  
 CC detection of increased expression of MDM2 gene products indicates  
 CC tumorigenesis.  
 XX  
 SQ Sequence 491 AA;  
 Query Match 99.3%; Score 550; DB 2; Length 491;  
 Best Local Similarity 99.1%; Pred. No. 7.6e-62;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTKVELVYLGQYIMTKRLYDEKQHHIVY 60  
 Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTKVELVYLGQYIMTKRLYDEKQHHIVY 76  
 Qy 61 CSNDLLGDLFGVPSFVKRHKIYTMIRNLVVNNQESSDSGTSVSEN 109  
 Db 77 CSNDLLGDLFGVPSFVKRHKIYTMIRNLVVNNQESSDSGTSVSEN 125  
 RESULT 11  
 AAW42879  
 ID AAW42879 standard; protein; 491 AA.  
 XX  
 AC AAW42879;  
 DT 30-APR-1998 (first entry)  
 XX  
 DE Amino acid sequence of human MDM2.  
 XX  
 KW MDM2; tumour; diagnosis; neoplasia; DNA binding protein; p53 polypeptide;  
 KW binding; tumour cell; p53-regulated growth; inhibition;  
 KW anti-cancer agent.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US5708136-A.  
 XX  
 PD 13-JAN-1998.  
 XX  
 PF 17-FEB-1995; 95US-00390516.  
 XX  
 PR 07-APR-1992; 92US-00867840.  
 PR 23-JUN-1992; 92US-00903103.  
 PR 07-APR-1993; 93US-00044619.  
 XX  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 PI Vogelstein B, Kinzler KW, Burrell M, Hill DE;  
 XX  
 DR WPI; 1998-100408/09.  
 XX  
 PT Human MDM2 binding polypeptide - comprises fragments of p53, useful in re  
 PT -establishing p53-regulated growth control in cells over-expressing MDM2.  
 XX  
 PS Disclosure; Col 23-28; 41pp; English.  
 XX  
 CC The present sequence represents human MDM2. The MDM2 gene is amplified in  
 CC some human tumours. The amplification of this gene is diagnostic of  
 CC neoplasia or its potential. It is speculated that the MDM2 protein is a  
 CC potential DNA binding protein that functions in the modulation of  
 CC expression of other genes and, when present in excess, interferes with  
 CC normal constraints on cell growth. A cell containing three recombinant  
 CC DNA constructs was produced. These constructs encode an MDM2 protein  
 CC fused to a sequence-specific DNA binding domain, a p53 polypeptide fused  
 CC to a transcriptional activation domain, and a reporter gene downstream  
 CC from a DNA element which is recognised by the sequence-specific DNA-

CC binding domain. The cell is used to identify a compound which interferes  
 CC with the binding of MDM2 and p53. Since MDM2 is overexpressed in tumour  
 CC cells and since binding of MDM2 to p53 appears to allow tumour cells to  
 CC escape from p53-regulated growth, compounds that inhibit such binding  
 CC would be useful as anti-cancer agents  
 XX  
 SQ Sequence 491 AA;  
 Query Match 99.3%; Score 550; DB 2; Length 491;  
 Best Local Similarity 99.1%; Pred. No. 7.6e-62;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTKVELVYLGQYIMTKRLYDEKQHHIVY 60  
 Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTKVELVYLGQYIMTKRLYDEKQHHIVY 76  
 Qy 61 CSNDLLGDLFGVPSFVKRHKIYTMIRNLVVNNQESSDSGTSVSEN 109  
 Db 77 CSNDLLGDLFGVPSFVKRHKIYTMIRNLVVNNQESSDSGTSVSEN 125  
 RESULT 12  
 AAW42971  
 ID AAW42971 standard; protein; 491 AA.  
 XX  
 AC AAW42971;  
 DT 29-APR-1998 (first entry)  
 XX  
 DE Amino acid sequence of human MDM2.  
 XX  
 KW MDM2; tumour; diagnosis; neoplasia; DNA binding protein; p53 polypeptide;  
 KW binding; tumour cell; p53-regulated growth; inhibition;  
 KW anti-cancer agent.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US5702903-A.  
 XX  
 PD 30-DEC-1997.  
 XX  
 PF 13-NOV-1995; 95US-00557393.  
 XX  
 PR 07-APR-1992; 92US-00867840.  
 PR 23-JUN-1992; 92US-00903103.  
 PR 07-APR-1993; 93US-00044619.  
 PR 18-MAY-1994; 94US-00245500.  
 XX  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 PI Vogelstein B, Kinzler KW;  
 XX  
 DR WPI; 1998-076411/07.  
 XX  
 DR N-PSDB; AAV03607.  
 XX  
 PT Cell containing reporter construct containing human MDM2 and p53 genes -  
 PT for identifying compounds that interfere with binding of human MDM2 to  
 PT human p53, useful as anti-cancer agents.  
 XX  
 PS Disclosure; Coulmans 22-28; 37pp; English.  
 XX  
 CC The present sequence represents human MDM2. The MDM2 gene is amplified in  
 CC some human tumours. The amplification of this gene is diagnostic of  
 CC neoplasia or its potential. It is speculated that the MDM2 protein is a  
 CC potential DNA binding protein that functions in the modulation of  
 CC expression of other genes and, when present in excess, interferes with  
 CC normal constraints on cell growth. A cell containing three recombinant  
 CC DNA constructs was produced. These constructs encode an MDM2 protein  
 CC fused to a sequence-specific DNA binding domain, a p53 polypeptide fused  
 CC to a transcriptional activation domain, and a reporter gene downstream  
 CC from a DNA element which is recognised by the sequence-specific DNA-  
 CC binding domain. The cell is used to identify a compound which interferes  
 CC with the binding of MDM2 and p53. Since MDM2 is overexpressed in tumour

CC cells and since binding of MDM2 to p53 appears to allow tumour cells to  
 CC escape from p53-regulated growth, compounds that inhibit such binding  
 CC would be useful as anti-cancer agents

SQ Sequence 491 AA;

Query Match 99.3%; Score 550; DB 2; Length 491;  
 Best Local Similarity 99.1%; Pred. No. 7.6e-62;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYLQYIMTKRLYDEKQOHIVY 60  
 DB 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYLQYIMTKRLYDEKQOHIVY 76  
 QY 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVNVNQSSDSGTSVSEN 109  
 DB 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVNVNQSSDSGTSVSEN 125

RESULT 13  
 AAW94304  
 ID AAW94304 standard; protein; 491 AA.  
 AC AAW94304;  
 XX 13-APR-1999 (first entry)  
 DT Human MDM2.  
 DE Human; MDM2; p53; tumorigenesis; growth regulation; diagnosis;  
 KW malignant fibrous histiocytoma; MFH; liposarcoma.  
 XX Homo sapiens.  
 OS US5858976-A.  
 PN 12-JAN-1999.  
 PD 14-FEB-1997; 97US-00801718.  
 PF 07-APR-1992; 92US-00867840.  
 PR 23-JUN-1992; 92US-00903103.  
 PR 07-APR-1993; 93US-00044619.  
 PR 17-FEB-1995; 95US-00390515.  
 XX (UWJO ) UNIV. JOHNS HOPKINS.  
 PA Kinzler KW, Vogelstein B;  
 PI WPI; 1999-152105/13.  
 DR N-PSDB; AAX03947.  
 XX Inhibiting growth of tumour cells having MDM2 gene amplification - with  
 PT MDM2-binding p53 fragment.

Claim 1; Col 23-28; 41pp; English.  
 The present invention describes: (1) a method for inhibiting the growth  
 of tumour cells which contain a human MDM2 gene amplification, comprising  
 administering to the cells a DNA molecule that expresses a polypeptide  
 consisting of a portion of p53 i.e. amino acids 13-41 of the 64 amino  
 acid sequence given in AAW94303, the polypeptide being capable of binding  
 to human MDM2 (the present sequence); (2) a method as in (1) where the  
 polypeptide lacks the homo-oligomerisation domain of p53; and (3) a  
 method as in (1) where the polypeptide lacks amino acids 138-393 of p53.  
 The method is useful for treating the following tumour types which have a  
 MDM2 gene amplification: M-7 malignant fibrous histiocytoma (MFH), M-20  
 MFH, L-9 liposarcoma, K17 liposarcoma, KL28 liposarcoma, KL30  
 liposarcoma, and OSA-CL MFH

SQ Sequence 491 AA;

Query Match 99.3%; Score 550; DB 2; Length 491;

Best Local Similarity 99.1%; Pred. No. 7.6e-62;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYLQYIMTKRLYDEKQOHIVY 60  
 DB 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYLQYIMTKRLYDEKQOHIVY 76  
 QY 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVNVNQSSDSGTSVSEN 109  
 DB 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVNVNQSSDSGTSVSEN 125

RESULT 14  
 AAY96567  
 ID AAY96567 standard; protein; 491 AA.  
 AC AAY96567;  
 XX 12-SEP-2000 (first entry)  
 DT MDM2 oncoprotein.  
 DE hEST2; telomerase; catalytic subunit; reverse transcriptase; life-span;  
 KW retinoblastoma; p53; tumour suppressor; inhibitor; arteriosclerosis;  
 KW proliferation; immortal; tumour therapy; macular degeneration; activator;  
 KW INK4; MDM2; oncoprotein.  
 XX Homo sapiens.  
 OS WO200001238-A2.  
 PN 02-JUN-2000.  
 PD 24-NOV-1999; 99WO-US027907.  
 PF 25-NOV-1998; 98US-0109891P.  
 PR 17-FEB-1999; 99US-0120549P.  
 XX (GENE-) GENETICA INC.  
 PA Hannon GJ, Beach DH;  
 PI WPI; 2000-400055/34.  
 DR N-PSDB; AAA29389.  
 XX New method for increasing the proliferative capacity of cell lines  
 PT comprises administering agents reversibly activating telomerase activity  
 PT and reversibly inactivating Rb/INK4 and/or p53 pathways useful in  
 PT treating age related diseases.

Claim 5; Page 120; 123pp; English.

The invention concerns methods and reagents for extending the life-span,  
 e.g. the number of mitotic divisions, of a cell. The method relies on  
 activation of a telomerase activity and inhibition of one or both of a  
 retinoblastoma (Rb)/INK4 pathway or a p53 pathway. Phosphorylation of Rb  
 by cyclin-dependent kinases, cdk4 and cdk6, releases the cells into the  
 division cycle. Binding of INK4 family members, e.g. the tumour  
 suppressor p16INK4a, inhibits kinase activity and results in growth  
 arrest. Rb inactivators can selectively and reversibly inactivate an  
 Rb/INK4 pathway, especially an Rb/p16INK4a pathway. The oncoprotein MDM2  
 is a cellular inhibitor of Rb/E2F function and the p53 tumour suppressor  
 and can also be used in the methods. Other molecules which can be used  
 include cdk4 or cdk6 mutants. In particular, a cdk4 mutant is one which  
 differs from at one or more of residues K22, R24, H95 and/or D97.  
 Additional constructs include a papilloma virus E7 protein, or other  
 viral oncoprotein which bypasses Rb and/or p53. Antisense constructs of  
 the Rb and p16INK4a genes may also be used. The methods are useful for  
 increasing the proliferative capacity of cells. The cells are  
 subsequently of use in pharmaceutical and cosmetic preparations used to  
 treat conditions related to (premature) ageing, e.g. macular degeneration  
 and arteriosclerosis. The cells can also be used to replace tumour cell  
 lines in vitro and for studies on biochemical and physiological aspects

